

(19) World Intellectual Property  
Organization  
International Bureau



(43) International Publication Date  
1 April 2004 (01.04.2004)

PCT

(10) International Publication Number  
**WO 2004/026888 A2**

(51) International Patent Classification<sup>7</sup>: C07H  
(21) International Application Number: PCT/US2003/029577  
(22) International Filing Date:  
19 September 2003 (19.09.2003)  
(25) Filing Language: English  
(26) Publication Language: English  
(30) Priority Data:  
60/412,479 19 September 2002 (19.09.2002) US

(71) Applicants (for all designated States except US): COLEY PHARMACEUTICAL GMBH [DE/DE]; Elisabeth-Selbert-Strasse 9, 40764 Langenfeld (DE). UNIVERSITY OF SASKATCHEWAN [CA/CA]; Kirk Hall, 117 Science Place, Saskatoon, Saskatchewan S7N 5C8 (CA). QIAGEN GMBH [DE/DE]; Max-Volmer-Strasse 4, 40724 Hilden (DE).

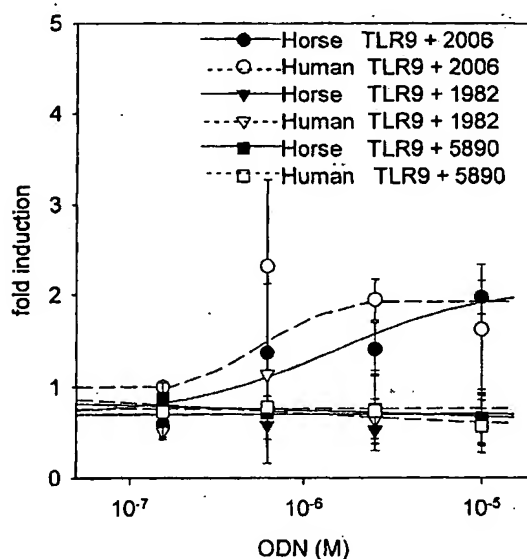
(72) Inventors; and  
(75) Inventors/Applicants (for US only): LIPFORD, Grayson, B. [US/US]; 38 Bates Road, Watertown, MA 02472 (US). MOOKHERJEE, Neeloffer [IN/CA]; Apt 408, 2233 Allison Road, Vancouver, BC V6T 1T7 (CA). BABIUK, Lorne [CA/CA]; 245 East Place, Saskatoon, Saskatchewan S7J 2Y1 (CA). BROWNLIE, Robert [CA/CA]; 123 O'Brien Crescent, Saskatoon, Saskatchewan S7K 5K3 (CA). GRIEBEL, Phillip [CA/CA]; Box 36, RR5, Saskatoon, Saskatchewan S7K 3J8 (CA). MUTWIRI, George [CA/CA]; 569 Nordstrum Road, Saskatoon, Saskatchewan S7K 7X6 (CA). HECKER, Rolf [DE/DE]; Benrodestr. 60, 40597 Düsseldorf (DE).

(74) Agent: STEELE, Alan, W.; Wolf, Greenfield & Sacks, P.C., 600 Atlantic Avenue, Boston, MA 02210 (US).

(81) Designated States (national): AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX,

[Continued on next page]

(54) Title: TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES



(57) Abstract: Novel amino acid and nucleotide sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) Toll-like receptor 9 (TLR9) are provided. Also provided are amino acid and nucleotide sequences for dog (canine), cat (feline), mouse (murine), and human TLR9. Comparison of these sequences, especially in combination with functional assessment for species-specific CpG motif preferences, permits identification of specific regions and amino acid residues of interest in TLR9 ligand interaction. Novel chimeric TLR9 receptor molecules, cells expressing these molecules, and methods for their use in screening assays for TLR9 ligands are also provided.

WO 2004/026888 A2



MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

**Published:**

— without international search report and to be republished upon receipt of that report

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO,

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

## TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

### Background of the Invention

Synthetic oligodeoxynucleotides (ODN) and DNA containing immunostimulatory CpG motifs (CpG DNA) function as potent adjuvants and activators of the innate immune system. Heeg K et al. (2000) *Int Arch Allergy Immunol* 121:87-97; Krieg AM (2001) *Vaccine* 19:618-22. A wide variety of CpG-containing sequences have been screened for biological activity and it is reported that optimal CpG DNA sequences can vary among species. Rankin R et al. (2001) *Antisense Nucleic Acid Drug Dev* 11:333-40.

Toll-like receptor 9 (TLR9) has recently been identified as a receptor for CpG ODN. Hemmi H et al. (2000) *Nature* 408:740-5. The molecular mechanism by which TLR9 recognizes CpG DNA is not understood.

### Summary of the Invention

Toll-like receptor 9 (TLR9) is known to be involved in innate immunity and to signal in response to CpG DNA. To date, the amino acid sequences only of human and murine TLR9 have been reported, and, interestingly, these two species are known to prefer different CpG motifs. The structural basis for this species-specific CpG motif preference has not yet been fully elucidated. The instant invention provides, in part, novel amino acid and nucleotide sequences of rat, pig, cow, and horse TLR9. These novel TLR9 sequences are useful for elucidating certain key structural features of TLR9. Specifically, comparison of sequences of murine, human, and these novel TLR9 sequences permits identification of areas of highly conserved sequence, areas of group conservation, and areas of hypervariability. In addition, such comparisons permit an assessment of evolutionary relatedness among TLR9 molecules of the various species, as well as an assessment of inter-species homologies. Importantly, such comparisons permit a rational basis for identifying amino acids in TLR9 that may be involved in the CpG binding site, as well as amino acids involved in conferring species specificity for particular CpG motifs. Such information may be used to design and construct novel TLR9 molecules which incorporate specific point or regional mutations and which possess desired ligand binding characteristics. Such information may also be useful in designing and identifying novel ligands for TLR9 of a given species.

- 2 -

In one aspect, the invention provides isolated polypeptides having amino acid sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) TLR9 polypeptides. These amino acid sequences correspond to SEQ ID NOs 1, 5, 9, 13, and 17, respectively. Each of these sequences is believed to include at least a majority of an extracellular domain, as well as a transmembrane region and at least part of a TLR/IL-1 receptor (TIR) domain. To the extent any such sequence may lack an amino-terminal and/or carboxy-terminal sequence, such sequence is ascertainable, without undue experimentation, using conventional molecular biology techniques and the sequence information provided herein.

In another aspect the invention provides isolated polypeptides having amino acid sequences for essentially the whole extracellular domain, optionally including a signal peptide, of each of rat, porcine, bovine, equine, and ovine TLR9. These amino acid sequences correspond to SEQ ID NOs 2, 6, 10, 14, and 18, respectively. Such extracellular domains are believed to include sequence specifically involved in binding to TLR9 ligand, such as CpG DNA. In addition, such extracellular domains are believed to include sequence that confers species specificity for particular CpG motifs.

Isolated nucleic acid molecules encoding the polypeptides just described above are also provided according to further aspects of the invention. Such nucleic acid molecules include, but are not limited to, nucleic acid molecules having sequences provided by SEQ ID NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively. Isolated nucleic acid molecules encoding the TLR9 polypeptides of SEQ ID NOs 1, 5, 9, 13, 17; and 2, 6, 10, 14, and 18 also include nucleic acid molecules that differ in sequence from SEQ ID NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively, due to degeneracy of the genetic code. Such nucleic acid molecules will hybridize, under stringent conditions, with suitably selected nucleic acid molecules having sequences selected from SEQ ID NOs 3, 4, 7, 8, 11, 12, 15, 16, 19, and 20.

In another aspect the invention provides a vector which includes an isolated nucleic acid molecule of the invention. In one embodiment the vector is an expression vector and the isolated nucleic acid molecule of the invention is operably linked to a regulatory sequence in the vector. When present within a cell, an expression vector according to this aspect of the invention causes the cell to express a polypeptide of the invention.

The invention according to another aspect provides a cell in which a vector of the invention is present. In one embodiment the cell containing the vector expresses a



- 3 -

polypeptide of the invention. In certain embodiments the cell also contains a reporter construct that transduces a TLR9-mediated signal in response to contact of the polypeptide of the invention or a TLR9 with a suitable TLR9 ligand. The cell containing the vector, and optionally containing the reporter construct, can be used in screening methods also provided by the invention.

In yet another aspect the invention provides an antibody or antibody fragment that binds specifically to an isolated polypeptide of the invention. In certain embodiments the antibody or antibody fragment binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide. More specifically, the antibody or antibody fragment binds uniquely to one of the isolated polypeptides of the invention. In one embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide also binds to either mouse or human TLR9. In another embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide does not also bind to either mouse or human TLR9. In some embodiments the antibody or antibody fragment binds selectively to a chimeric TLR9 polypeptide of the invention. In certain embodiments the antibody or antibody fragment of the invention is a monoclonal antibody or fragment of a monoclonal antibody.

In one aspect the invention provides a method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the first species. The method involves aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species; generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

- 4 -

In another aspect the invention provides a method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9. The method according to this aspect of the invention involves aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a CpG DNA optimized for murine TLR9; generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids. In one embodiment the method according to this aspect of the invention is performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred CpG DNA).

In another aspect the invention also provides an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (extracellular domain (ECD) of murine TLR9) except for substitution of at least one key amino acid identified according to the method above. The polypeptide according to this aspect of the invention is a chimeric TLR9 polypeptide. Preferably the polypeptide according to this aspect of the invention binds to CpG DNA optimized for human TLR9 better than does the isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (ECD of murine TLR9). In one embodiment the polypeptide includes only one substituted amino acid. The isolated polypeptide according to this aspect of the invention may further include sequence involved in TLR/IL-1R signal transduction, e.g., intracellular domain of TLR9 as provided in SEQ ID NOs 29 and 33. For example, in one embodiment a polypeptide according to this aspect of the invention is an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:29 (full length murine TLR9) except for substitution of at least one key amino acid identified according to the method above.

- 5 -

In another aspect the invention provides an isolated nucleic acid molecule including a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described. In one embodiment the isolated nucleic acid molecule has a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described.

5 In yet another aspect, the invention provides a screening method to identify a TLR9 ligand. The method involves contacting a polypeptide (including a chimeric TLR9 polypeptide) of the invention with a candidate TLR9 ligand; measuring a signal in response to the contacting; and identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling. In one embodiment  
10 the candidate TLR9 ligand is an immunostimulatory nucleic acid. In one embodiment the candidate TLR9 ligand is a CpG DNA.

The invention also provides, in yet a further aspect, a screening method to identify species-specific CpG-motif preference of an isolated polypeptide of the invention. The method according to this aspect of the invention involves contacting an isolated polypeptide  
15 of the invention with a CpG DNA including a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG; measuring a signal in response to the contacting; and identifying a species-specific CpG-motif preference when the signal in  
20 response to the contacting is consistent with TLR9 signaling. In one embodiment the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

	TCCATGACGTTTTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTTTTGATGTT	(SEQ ID NO:41),
25	TCCATTACGTTTTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTTTTGATGTT	(SEQ ID NO:43),
	TCCATGCCGTTTTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTTTTGATGTT	(SEQ ID NO:46),
30	TCCATGAAGTTTTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTTTTGATGTT	(SEQ ID NO:48),
	TCCATGACATTTTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTTTGATGTT	(SEQ ID NO:50),
	TCCATGACTTTTTTTGATGTT	(SEQ ID NO:51),
35	TCCATGACGCTTTTGTGTT	(SEQ ID NO:52),
	TCCATGACGATTTTTGATGTT	(SEQ ID NO:53),
	TCCATGACGGTTTTGATGTT	(SEQ ID NO:54),

- 6 -

TCCATGACGTCTTTGATGTT (SEQ ID NO:55),  
 TCCATGACGTATTTGATGTT (SEQ ID NO:56), and  
 TCCATGACGTGTTTGATGTT (SEQ ID NO:57).

In certain embodiments of the screening methods of the invention, the signal includes  
 5 expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway. In one  
 embodiment the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B. In one  
 embodiment the signal in response to contacting is binding of the candidate TLR9 ligand or  
 CpG DNA to the polypeptide of the invention.

In one embodiment the screening method is performed on a plurality of test  
 10 compounds. In one embodiment the response mediated by the TLR9 signal transduction  
 pathway is measured quantitatively and the response mediated by the TLR9 signal  
 transduction pathway associated with each of the plurality of test compounds is compared  
 with a response arising as a result of an interaction between the functional TLR9 and a  
 reference immunostimulatory compound.

15

### Brief Description of the Figures

Figure 1 depicts a Clustal W multiple sequence alignment of deduced amino acid  
 sequences for cat (feline), dog (canine), cow (bovine), mouse (murine), sheep (ovine), pig  
 (porcine), horse (equine), human, and rat TLR9 polypeptides. The deduced amino acid  
 20 sequences for feline, canine, bovine, murine, ovine, porcine, equine, human, and rat TLR9  
 polypeptides shown in the figure correspond to SEQ ID NOs 25, 21, 9, 29, 17, 5, 13, 33, and  
 1, respectively. Lines labeled "multiple" refer to the multiple sequence alignment of all six  
 sequences shown. Lines labeled "mo/hu" refer to a paired sequence alignment of mouse and  
 human TLR9 sequences alone.

25 Figure 2 is a cladogram depicting an evolutionary relatedness tree for rat, murine,  
 porcine, bovine, equine, and human TLR9 polypeptides in Figure 1.

Figure 3 is a graph depicting species specificity of TLR9 signaling with selected  
 oligonucleotides having strong specificity for human (2006), mouse (5890), or neither (1982).

30

### Detailed Description of the Invention

The present invention provides novel amino acid and nucleotide sequences for TLR9  
 derived from rat, pig, cow, horse, and sheep. These sequences can be used to identify key  
 features of the primary sequences of these and related TLR molecules, including previously

- 7 -

known primary sequences of human and mouse (murine) TLR9. Such key features include binding site information and species specificity toward particular CpG motifs. Native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to identify and to design novel TLR9 ligands. Additionally, the native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to compare various TLR9 ligands, including CpG DNA.

In one aspect the invention provides isolated TLR9 polypeptides, and isolated nucleic acid molecules encoding them, from rat, pig, cow, horse, and sheep. The term "isolated" as used herein with reference to a nucleic acid molecule or polypeptide means substantially free of or separated from components with which it is normally associated in nature, e.g., other nucleic acids, proteins, lipids, carbohydrates or *in vivo* systems to an extent practical and appropriate for its intended use. In particular, the nucleic acids or polypeptides are sufficiently pure and are sufficiently free from other biological constituents of host cells so as to be useful in, for example, producing pharmaceutical preparations. Because an isolated nucleic acid or polypeptide of the invention may be admixed with a pharmaceutically acceptable carrier in a pharmaceutical preparation, the nucleic acid or polypeptide may represent only a small percentage by weight of such a preparation. The nucleic acid or polypeptide is nonetheless substantially pure in that it has been substantially separated from the substances with which it may be associated in living systems.

An amino acid sequence of rat TLR9 is provided as SEQ ID NO:1. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:1 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of rat TLR9 (See Figure 1). Amino acids numbered 1-821 of SEQ ID NO:1 are presumptively extracellular domain and correspond to SEQ ID NO:2. SEQ ID NO:3 is a nucleotide sequence of rat TLR9 cDNA having an open reading frame corresponding to nucleotides 1-3096. SEQ ID NO:4 is a nucleotide sequence of rat cDNA encoding amino acids 1-821 of SEQ ID NO:1.

An amino acid sequence of porcine TLR9 is provided as SEQ ID NO:5. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:5 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of porcine TLR9

- 8 -

(See Figure 1). Amino acids numbered 1-819 of SEQ ID NO:5 are presumptively extracellular domain and correspond to SEQ ID NO:6. SEQ ID NO:7 is a nucleotide sequence of porcine TLR9 cDNA having an open reading frame corresponding to nucleotides 77-3166. SEQ ID NO:8 is a nucleotide sequence of porcine cDNA encoding amino acids 1-819 of SEQ ID NO:5.

An amino acid sequence of bovine TLR9 is provided as SEQ ID NO:9. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:9 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of bovine TLR9.

(See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:9 are presumptively extracellular domain and correspond to SEQ ID NO:10. SEQ ID NO:11 is a nucleotide sequence of bovine TLR9 cDNA having an open reading frame corresponding to nucleotides 84-3170. SEQ ID NO:12 is a nucleotide sequence of bovine cDNA encoding amino acids 1-818 of SEQ ID NO:9.

An amino acid sequence of equine TLR9 is provided as SEQ ID NO:13. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:13 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of equine TLR9 (See Figure 1). Amino acids numbered 1-820 of SEQ ID NO:13 are presumptively extracellular domain and correspond to SEQ ID NO:14. SEQ ID NO:15 is a nucleotide sequence of equine TLR9 cDNA having an open reading frame corresponding to nucleotides 115-3207. SEQ ID NO:16 is a nucleotide sequence of equine cDNA encoding amino acids 1-820 of SEQ ID NO:13.

An amino acid sequence of ovine TLR9 is provided as SEQ ID NO:17. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:17 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of ovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:17 are presumptively extracellular domain and correspond to SEQ ID NO:18. SEQ ID NO:19 is a nucleotide sequence of ovine TLR9 cDNA having an open reading frame corresponding to nucleotides 92-3178. SEQ ID NO:20 is a nucleotide sequence of ovine cDNA encoding amino acids 1-818 of SEQ ID NO:17.

## SEQ ID NO:1 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAEPRSNITSLSLIANRI  
 HHLHNLDVHLPNVRQLNLKWCNPPPGLSPLHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLNL  
 5 SHTNILLVDASSLAGLHSLRVLFMDGNCYYKNPCNGAVNVTDAFLGLSNLTHLSLKYNLTVPRQLPPSLEYL  
 LLSYNLIVKLGAEDLANLTSRLMDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLSHLEGLVLKDSLSHSLN  
 SKWFQGLANLSVLDLSENFYIESINKTSFQNLTRLRKLDSLNYCKKVSFARLHLASSFKSLVSLQELNMNGIF  
 FRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGV  
 PASLTPALPSTPVSKNFMVRCKNLRFMDLSRNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK  
 10 VLDLSYNKLDLYHKSFSSELPQLQALDLSYNSQPFMSQGIHNFSLANLSRLQNLSLAHNDIHSRVSSRLYSTS  
 VEYLDPSGNGVGRMWDEEDLYLYFFQDLRSLIHLDSLQNKHLILRPQNLNLYLPKSLTKLSFRDNHLSFFNWSSIA  
 FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVPAPFALAVELKEVNLSHNILKTVDRSWFGPIV  
 MNLTVDVSSNPLHCACGAPFVDLLLEVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFGLSLL  
 AVAVGTVPPLQLHLCGWDVWYCFHLCLAWPLPLTRGRRSAQALPYDAFVVFDDKAQSAVADWVYNELRVRLERRG  
 15 RRALRLCLEDRDWLPQTLFENLWASIYGSRKTLFVLAHTDKVSGLLRTSFLLAQQRLLEDKRDVVVLVILRPDA  
 HRSRYVRLRQLRCLQSVLFWPHQPNGQGSFWAQLSTALTRDNHNFYNRNFCRGPTAE

## SEQ ID NO:2 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAEPRSNITSLSLIANRI  
 HHLHNLDVHLPNVRQLNLKWCNPPPGLSPLHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLNL  
 20 SHTNILLVDASSLAGLHSLRVLFMDGNCYYKNPCNGAVNVTDAFLGLSNLTHLSLKYNLTVPRQLPPSLEYL  
 LLSYNLIVKLGAEDLANLTSRLMDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLSHLEGLVLKDSLSHSLN  
 SKWFQGLANLSVLDLSENFYIESINKTSFQNLTRLRKLDSLNYCKKVSFARLHLASSFKSLVSLQELNMNGIF  
 FRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGV  
 25 PASLTPALPSTPVSKNFMVRCKNLRFMDLSRNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK  
 VLDLSYNKLDLYHKSFSSELPQLQALDLSYNSQPFMSQGIHNFSLANLSRLQNLSLAHNDIHSRVSSRLYSTS  
 VEYLDPSGNGVGRMWDEEDLYLYFFQDLRSLIHLDSLQNKHLILRPQNLNLYLPKSLTKLSFRDNHLSFFNWSSIA  
 FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVPAPFALAVELKEVNLSHNILKTVDRSWFGPIV  
 MNLTVDVSSNPLHCACGAPFVDLLLEVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFG  
 30

## SEQ ID NO:3 (Rat TLR9)

atgggtctctgtcgaggaccctgcaccccttgcctctcctggtacagggccgcagtgctggctgaggctctggcc  
 ctgggtaccctgectgccttctaccctgtgaactgaagcctcatggcctggtagactgcaactggctcttctctg  
 aagctctgtgcctcacttctctgccgcagaacccggtccaacatcaccagccttctccttgatcgccaaccgcac  
 35 caccacctgcacaacctcgacttctgtccacctgccccacgtgcgacagctgaacctcaagtggaaactgtccgccc  
 cctggcctcagcccttgcacttctcctgccgcatgaccattgagcccaaaccttctcctggctatgcgcatgctg  
 gaagagctgaacctgagctataacggtatcaccactgtgccccgcctgccagctccctgaagaatctgagccta  
 agccacaccaacatcctggtactcgatgccagcagcctcgctggcctgcacagcctgcgagttctcttcatggac  
 gggaaactgctactacaagaacccctgcaacggggcggtgaacgtgaccccggaagccttctcctgggcttgagcaac  
 40 ctacccacttgccttaagtataacaacctcacagaggtgccccgcaactgccccccagcctggagtgacctc  
 ctgctgtcctataaacctcatcgtaagctggggggcggaagacctagccaacctgacctcccttcgaatgcttgat  
 gtgggtgggaattgcccgtcgctgtgatcacgccccgacctctgtacagaatgccggcgagaagtcccttgatctg  
 caccctcagactttccatcacctgagccacctgaaggcctgggtgctgaaggacagttctctccactcgctgaac  
 tccaagtgggtccagggtctggcgaaacctctcggtgctggacctgaagcgagaactttctctacgagagcatcaac  
 45 aaaaccagcgcttccagaacctgacctgctgcgcaagctcgacctgtccttcaattactgcaagaaggatctg  
 ttcgccccgctccacctggcaagttccttcaagagcctgggtgctgctgacaggagctgaacatgaacggcatctt  
 ttccgcttactcaacaagaacacgctcaggtggctggctggctctgccccagctccacacgctgcaccttcaaatg  
 aatttcatcaaccaggcgagctcagcgctcttagtaccttccagaccttgccttctgtggaccttccaataat  
 cgcattcagcgggcctccaacgctgtccagagctgccccgaaaaggcagacgaggcggaaggggggtccatgg  
 50 cctgcaagctcaccacagctctcccagcactcccgctctcaagaacttcatgggtcaggtgtaagaacctcaga  
 ttcaccatggacctgtctcggaacaaccaggtgactatcaagccagagatgttcgtcaacctctccatctccag  
 tgtctgagcctgagccacaactgcacgagcaggtgtcaatggctctcagttcctgcccgtgaccaacctgaag  
 gtgctggacctgtcctataacaagctggacctgtaccattcgaaatcggtcagtgagctcccacaggtgcaggcc

- 10 -

ctggacctgagctacaacagccagccattcagcatgcaggggataggccacaacttcagttttctggccaatctg  
tccaggttacagaaccttagcctggcacacaatgacattcacagccgctgtcctcacgcctctacagcacctca  
gtggagtatctggacttcagcggcaacgggtgtgggcccgcagtggtggacgaggaggacctttacctctattttcttc  
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaacctcaac  
5 tacctccccaagagcctgacgaagctgagtttccgtgacaatcacctctctttctttaactggagcagtctggcc  
ttcctgcccattctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgccta  
ggcagctcctccagaaactggatgtcagtagcaacagtatcgtctttgtgggtcccagcctctcttgcctctggcg  
gtagactctaaaagaggtcaacctcagccataacatcctcaagactgtggatcgctcctgggtttgggcccattgtg  
atgaacctgacggttctagacgtgagcagcaacctctgcattgtgcctgcggtgcaccttctgtagacttactg  
10 ctggaagtgcagaccaaggtgcctggcctggctaacgggtgtgaagtgtggcagtcctccgcccagctgcagggccgc  
agcatctttgcgaagacctgcggctgtgcctggatgacgtcctttctcgggactgctttggcctttcactcctg  
gctgtggccgtgggcaacgggtgttgcctttactgcagcatctctgcggctgggacgtctggtactgtttccatctg  
tgcttgccatggtctacctttgctgacctgtggcggcgagcgcccaagctctccttatgatgccttcgtgggtg  
ttcgataaggcgagagcgcggttgcctgactgggtgtataacgagcttcgagtgcggttagaggagcgggcgcggt  
15 cgccgagccctacgcttgtgtctggaggaccgagattggctgcctggccagacactcttcgagaacctctgggccc  
tccatctatggcagccgcaagactctgtttgtgctggccacacggaacaaggctcagtgccctctgcgcaccagc  
ttcctgctggctcagcagcgctgctggaggaccgcaaggacgtgggtgttgggtgatcctgcgcctgatgcc  
caccgctcccgtacgtgcgactgcgccagcgctctgcgccagagtgctcttctggccccatcagcccaac  
gggcagggcagcttctgggcccagctgagtacagccctgactagggacaaccaccacttctataaccggaacttc  
20 tgcgggggacctacagcagaatag

## SEQ ID NO:4 (Rat TLR9)

atgggtctctgtcgcaggacctgcaccccttgtctctcctggtagaggccgagtgctggctgaggtctctggcc  
ctgggtacctgctgccttctaccctgtgaactgaagcctcatggcctggttagactgcaactggctcttccctg  
25 aagtctgtgctcacttctctgcccagaaacccggttccaacatcaccagcctttccttgatcgccaaccgcac  
caccacctgcacaacctcgacttctgccaacctgccaacgtgcgacagctgaacctcaagtggaaactgtccgccc  
cctggcctcagcccttgcaacttctcctgcccagatgaccattgagcccaaaccttccctggctatgcgcattgtg  
gaagagctgaacctgagctataacggtatcaccactgtgccccgcctgccagctccctgacgaatctgagccta  
agccacaccaacatcctggtactcgatgccagcagcctcgctggcctgcacagcctgcgagttctcttcatggac  
30 gggaaactgctactacaagaacccctgcaacggggcggtgaacgtgaccccgagccttctgggcttgagcaac  
ctcaccactgttcccttaagtataacaacctcacagaggtgccccgcaactgccccccagcctggagtagctc  
ctgctgtcctataacctcatcgtcaagctgggggcccgaagacctagccaacctgacctcccttcgaatgcttgat  
gtgggtgggaattgcccgtcgctgtgatcacgccccgacctctgtacagaatgcccgcagaagtcccttgatctg  
cacctcagacttccatcacctgagccaccttgaggcctgggtgctgaaggacagttctctccactcgctgaac  
35 tccaagtgttccagggtctggcgaaacctctcggtgtggacctgaagcgagaacttctctcagagagcatcaac  
aaaaccagcgcttccagaacctgacctgctgcgaagctcgacctgtccttcaattactgaagaaggatctg  
ttcgcccgctccacctggcaagttccttcaagagcctgggtgtcgctgcaggagctgaacatgaacggcatcttc  
ttccgcttactcaacaagaacacgctcaggtggctgggtgtgcccgaagctccacacgctgcaccttcaaatg  
aatctcatcaaccaggcgagctcagcgtctttagtaccttccgagcccttcgctttgtggacctgtccaataat  
40 cgcacagcgggctcccaacgctgtccagagtcgccccgaaaaggcagacgaggcgagaaaggggttccatgg  
cctgcaagctcacccccagctctcccagcactcccgctctcaaagaacttcatggctcaggtgtaagaacctcaga  
ttcaccctgacctgtctcggaacaaccaggtgactatcaagccagagatgttcgtcaaccttcccatctccag  
tgtctgagcctgagccacaactgcacgcgaggtgtcaatggctctcagttcctgcccgtgaccaacctgaag  
gtgctggacctgtcctataacaagctggacctgtaccattcgaaatcggttcagtgagctcccacagttgcaggcc  
45 ctggacctgagctacaacagccagccattcagcatgcaggggataggccacaacttcagttttctggccaatctg  
tccaggttacagaaccttagcctggcacacaatgacattcacagccgctgtcctcacgcctctacagcacctca  
gtggagtatctggacttcagcggcaacgggtgtgggcccgcagtggtggacgaggaggacctttacctctattttcttc  
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaacctcaac  
tacctccccaagagcctgacgaagctgagtttccgtgacaatcacctctcttctttaactggagcagctctggcc  
50 ttccgtcccattctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgcctg  
ggcagctcctccagaaactggatgtcagtagcaacagtatcgtctttgtgggtcccagccttcttgcctctggcg  
gtagagctaaaagaggtcaacctcagccataacatcctcaagactgtggatcgctcctgggtttgggcccattgtg  
atgaacctgacggttctagacgtgagcagcaacctctgcattgtgcctgcggtgcaccttctgtagacttactg  
ctggaagtgcagaccaaggtgcctggcctggctaacgggtgtgaagtgtggcagtcctccgcccagctgcagggccgc  
55 agcatctttgcgaagacctgcggctgtgcctggatgacgtcctttctcgggactgctttggc



- 11 -

## SEQ ID NO:5 (Porcine TLR9)

MGPRCTLHPLSLLVQVTALAAALAQGRLPAPFLPCELQPHGLVNCNWFLKSVPHFSAAAPRANVTSLSLLSNRIH  
HLHDSDFVHLSSLRTLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNSITTPALPDSLVSLSLS  
RTNILLVLDPTHLTGLHALRYLYMDGNCYYKNPCQGALEVVPGALLGLGNLTHLSLKYNNTLEVPRLPPSLETLL  
5 LSYNHIVTLTPEDLANLTALRVLDVGGNCRCDHARNPCRECPKDHPKLHSDTFSHLSRLEGLVLKDSLSLYNLD  
RWFRGLDRLQVLDLSENFLYDCITKTAFQGLARLSLNLNFYHKKVSFAHLHLAPSFHGLRSLKELDMHGIF  
RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLYVDLSDNRISGAARPVAITREVDGRERVWLP  
NLAPRPLDTRLSEDFMPNCKAFSFTLDLSRNNLVITIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRV  
10 DLSHNKLDLYHGSRFTLPRLEALDLSYNSQPFMTQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSQQLCSASLC  
ALDFSGNDLSRMWAEGDLYLRFFQGLRSLVWLDLSQNLHHTLLPRALDNLPKSLKHLHLRDNNAFFNWSLTLL  
PKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN  
LKVLVDVSANPLHCACGATFVGFLLEVQAAVPGLPSPVKCGSPGQLQGHSTFAQDLRLCLDETLSWNCFGISLLAM  
ALGLVVPMLHLCGWDLWYCFHLCIAWLPHRGQRGADALFYDAFVVFDAQSAVADWVYNELRVQLEERRGRRA  
LRLCLEERDNLPGKTLFENLWASVYSSRKTFLVLAHTDRVSGLLRASFLLAQQRLLLEDKDVVVLVILRPDAYRS  
15 RYVRLRQRLCRQSVLLWPHQPRGQGSFWAQLGTALTRDNHFFYNRNFCRGPTTAE

## SEQ ID NO:6 (Porcine TLR9)

MGPRCTLHPLSLLVQVTALAAALAQGRLPAPFLPCELQPHGLVNCNWFLKSVPHFSAAAPRANVTSLSLLSNRIH  
HLHDSDFVHLSSLRTLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNSITTPALPDSLVSLSLS  
20 RTNILLVLDPTHLTGLHALRYLYMDGNCYYKNPCQGALEVVPGALLGLGNLTHLSLKYNNTLEVPRLPPSLETLL  
LSYNHIVTLTPEDLANLTALRVLDVGGNCRCDHARNPCRECPKDHPKLHSDTFSHLSRLEGLVLKDSLSLYNLD  
RWFRGLDRLQVLDLSENFLYDCITKTAFQGLARLSLNLNFYHKKVSFAHLHLAPSFHGLRSLKELDMHGIF  
RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLYVDLSDNRISGAARPVAITREVDGRERVWLP  
25 NLAPRPLDTRLSEDFMPNCKAFSFTLDLSRNNLVITIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRV  
DLSHNKLDLYHGSRFTLPRLEALDLSYNSQPFMTQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSQQLCSASLC  
ALDFSGNDLSRMWAEGDLYLRFFQGLRSLVWLDLSQNLHHTLLPRALDNLPKSLKHLHLRDNNAFFNWSLTLL  
PKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN  
LKVLVDVSANPLHCACGATFVGFLLEVQAAVPGLPSPVKCGSPGQLQGHSTFAQDLRLCLDETLSWNCFG

## 30 SEQ ID NO:7 (Porcine TLR9)

gagcacgaacatccttcactgtagctgctgcccggctctgccagccagacccttggagaagacccccactccctgt  
catgggcccccgctgcaccctgcacccctttctctcctggctgcaggtgacagcgctggctgcggctctggccca  
gggcaggtgctgccttcctgcctgtgagctccagccccagggcctggtagactgcaactggctcttcctgaa  
gtccgtgccccacttctcgggcgagcgccccgggccaacgtcaccagcctctccttactctccaaccgcatcca  
35 ccactgcacgactccgacttcgtccactgtccagcctacgaactctcaacctcaagtggaaactgcccgcggc  
tgccctcagccccatgcacttccctgccacatgaccatcgagcccaacaccttctggcctgcccaccctgga  
ggagctgaacctgagctacaacagcatcacgaactgctgcccctgcccagactccctcgtgctcctgtcgctgag  
ccgcaccaacatcctgggtgctagacccacccacctcactggcctacatgcctgcgctacctgtacatggatgg  
caactgctactacaagaacccctgccagggggcgctggaggtggtgcccgggtgccctcctcgccctgggcaacct  
40 cacacatctctcactcaagtacaacaatctcacggaggtgccccgcagcctgccccccagcctggagacctgct  
gttgctcctacaaccacattgtcacctgacgcctgaggacctggccaatctgactgccctgcgctgcttgatgt  
gggggggaactgccgcccgtgtgaccatgcccgcaacccctgcagggagtgcccaaaggaccacccaagctgca  
ctctgacaccttcagccacctgagccgctcgaaggcctgggtgtgaaagacagtctctctacaacctggacac  
caggtgggttccgagggcctggacaggtccaagtgtgacctgagtgagaacttctctacgactgcatcaccac  
45 gaccagggccttccagggcctggccgactgcgcagcctcaacctgtccttcaattaccacaagaaggtgtcctt  
tgccacctgcacctggcacctccttgggcacctccggtccctgaaggagctggacatgcatggcatcttctt  
ccgctcgctcagtgagaccacgctccaacctctgggtccaactgcctatgctccagacctgcgctgcagatgaa  
cttcattaaccaggccccagctcagcatcttggggccttccctggcctgctgtacgtggacctatcggaacacg  
catcagcggagctgcaaggccagtgccattactagggaggtggatggtagggagagggctggtgctgccttcag  
50 gaacctcgctccacgtccactggacactctccgctcagaggacttcatgccaaactgcaaggccttcagcttcac  
cttggaacctgtctcggaacaacctggtgacaatccagtcggagatgtttgctcgccctctcacgcctcgagtgcct  
gcgctgagccacaacagcatctccaggcggtcaatggctcagtttggcggctgaccagcctgcggggtgct  
ggacctgtcccacaacaagctggacctgtatcacggcgctcgttcacggagctgcccgcgctggaagcactgga  
cctcagctacaatagccagcccttaccatgcagggtgtgggccacaacctcagcttctggtggccagctgcccgc

- 12 -

cctgcgctacctcagcctggcgacacaatgacatccatagccgagtggtcccagcagctctgtagcgcctcactgtg  
 cgccctggacttttagcggaacgatctgagccggatgtgggctgagggagacctctatctccgcttcttccaagg  
 cctaagaagcctagtctggctggacctgtcccagaaccacctgcacaccctcctgccacgtgccctggacaacct  
 5 ccccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgacctcct  
 gcccagctggaaacctggacttggtggaaccagctgaaggccctaagcaatggcagcctgcatctggcac  
 ccagctgcgaggctggacctcagtggcaacagcatcggtttgtgaacctggcttcttgcctggccaagca  
 gttagaagagctcaacctcagcgccaatgccctcaagacagtggagccctcctgggttggctcgatgggtgggcaa  
 cctgaaagtcttagacgtgagcgccaacctctgcatctgctgtggggcgaccttcgtgggtcctctgtgga  
 10 ggtacaggctgacctgacctgggtgcccagcgcgtcaagtgtggcagtcggggcagctccaggccatagcat  
 ctttgcgcaagacctgcgcctctgctggatgagacctctcgtggaactgttttggcatctcgtgctggccat  
 ggccctgggctggttgtgcccctgctgcaccacctctgcggctgggacctctggtactgcttccacctgtgcct  
 ggctggtgccccaccgagggcagcgggcgggcgagcagccctgttctatgatgccttcgtggtctttgacaa  
 agctcagagtgtgtggcgactgggtgtacaacgagctgcggtgagctggaggagcgccgtggcgccgagc  
 actgcgcctgtgctggaggagcagactggttacctggcaagacgctcttcgagaacctgtgggctcagctcta  
 15 cagcagccgcaagacctgttgtgctggcccaagcagcagcgtgtcagcgccctcttgcgtgacagtttctgtg  
 ggccagcagcgctgctggaggacgcaaggacgttgttagtgctggtgatcctgcgccccgatgcctaccgctc  
 ccgctacgtgcggctgcccagcgctctgcgcccagagtgtcctcctctggccccaccagccccgtgggcaggg  
 cagcttctggggccagctgggcacagccctgaccagggaacaaccaccacttctataaccggaactctgcggggg  
 cccacgacagccgaatagcactgagtgcagccagctgtgccccagccccctggatttgcctctctgctgggg  
 20 tggcccaacctgtttgtctcagccacaccactgtctgtcctcgttccccacccccccccagcctggcatgt  
 aacatgtgccaataaatgtctaccggagggccaagaaaaaaaaaaaaaaaaaaaa

## SEQ ID NO:8 (Porcine TLR9)

atgggcccccgctgcacctgcaccccttctctcctgggtgcaggtgacagcgtggctgcggctctggcccag  
 25 ggcaggctgctgccttctgcctgtgagctccagccccagccctggtgaactgcaactggctcttctctgaag  
 tccgtgccccacttctcgccggcagcgccccggccaacgtcaccagcctctccttactctccaaccgcactcac  
 cacctgcacgactccgacttctccacctgtccagactcgaactctcaacctcaagtggaaactgcggcggt  
 ggctcagccccatgcacttccccgccacatgaccatcgagcccaacaccttctggccgtgcccacctggag  
 30 gagctgaacctgagctacaacagcatcacgacctgacctgacctgacctcctcgtgtcctgtcgctgagc  
 cgcaccaacatcctgggtgctagacccacccacctcactggcctacatgacctgcgctacctgtacatggatggc  
 aactgctactacaagaaccttgcagggggcgctggaggtggtgcccgtgacctcctcgccctgggcaacctc  
 acacatctctcactcaagtacaacaatctcacggagggtgccccgcagcctgccccccagcctggagacctgctg  
 ttgtctacaaccacttgtcacctgacgcctgaggacctggccaatctgactgacctgacctgacctgacctg  
 35 ggggggaactgcccggctgtgacctgccccgcaacctgcaaggagtgcccaaggaccacccccagctgcac  
 totgacaccttcagccacctgagccgctcgaaggcctgggtgtgaaagacagttctctctacaacctggacacc  
 aggtggttccgaggcctggacaggtcccaagtgtggacctgagtgagaacttctctacgactgcatcaccaag  
 accacggccttccagggcctggccgactgcgcagcctcaacctgtccttcaattaccacaagaagggtgtccttt  
 gccacctgcacctggcaccctcctttgggcacctccggctcctgaaggagctggacatgcatggcatcttcttc  
 40 cgctcgctcagtgagaccagctccaacctctggtccaactgectatgctccagacctgcgctgcagatgaac  
 ttcatataaccaggcccagctcagcatctttggggccttccccggcctgctgtacgtggacctatcggaacaaccgc  
 atcagcggagctgcaaggccagtgccattactagggagggtggatggtagggagagggtctggctgccttccagg  
 aacctcgctccacgtccactggacactctccgctcagaggacttcatgccaaactgcaaggccttcagcttcacc  
 ttggacctgtctcggaacaacctggtgacaatccagtcggagatgtttgtcgcctctcacgcctcgagtgcctg  
 45 cgctgagccacaacagcatctcccaggcggtcaatggctctcagtttgtgcccgtgaccagcctgcccgtgctg  
 gacctgtcccacaacaagctggacctgtatcacggcgctcggttcacggagctgcccgcctggaagcactggac  
 ctacgtacaatagccagccctttaccatgcagggtgtggggccacaacctcagcttcgtggccagctgcccgc  
 ctgacctacctcagcctggcgacacaatgacatccatagccgagtggtcccagcagctctgtagcgcctcactgtgc  
 gccctggacttttagcggaacgatctgagccggatgtgggctgagggagacctctatctccgcttcttccaaggc  
 ctaagaagccttagctggctggacctgtcccagaaccctgcacaccctcctgccacgtgccctggacaacctc  
 50 cccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgacctctg  
 cccaagctggaaacctggacttggtggaaccagctgaaggccctaagcaatggcagcctgccatctggcacc  
 cagctgcccagggtggacctcagtggaacagcatcggtttgtgaacctggcttcttgcctggccaagcag  
 ttagaagagctcaacctcagcgccaatgccctcaagacagtgagccctcctgggttggctcgatgggtgggcaac  
 ctgaaagtcttagacgtgagcgccaacctctgcactgtgacctgtggggcgaccttcgtgggttctctgctggag  
 55 gtacaggctgacctgacctgggtgcccagccgctcaagtgtggcagtcggggcagctccaggccatagcatc  
 tttgcgcaagacctgacctctgacctggatgagacctctcgtggaactgttttggc

- 13 -

## SEQ ID NO:9 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLTLPALPCELQPHGQVDCNWLFLKSVPHFSAAGAPRANVTSLSLISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTEIPNTFLAVPTLEELNLSYNGITTVPALPSSSLVLSLS  
5 HTSILVLGPTHFTGLHALRFLYMDGNCYMNPCCRALEVAPGALLGLGNLTHLSLKYNNTLEVPRLPPSLDTLL  
LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSISLYKLEK  
DWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNHYHKKVSFAHLHLASSFGSLVSLEKLDMHGIF  
RSLTNITLQSLTRLPLKQLSLHLQNLFINQAQLSIFGAFPSLLFVLDLSDNRISGAATPAAALGEVDSRVEVWRLPR  
GLAPGPLDAVSSKDFMPSCNLFNLTDLNRNLTITQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD  
10 LSHNKL DLYHGRSFTLPLQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSRLYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLNLPKSLRQLRLRDNNLAFFNWSSTVLP  
RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIPGFFVRATRLIELNLSANALKTVDPSWFGSLAGTL  
KILDVSANPLHCACGAAFVDFLLERQEA VPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETSLDCFGLSLLMVA  
LGLAVPMLHHL CGWDLWYCFHLCLAHLP RRRRQRGEDTLLYDAVVVFDKVQSAVADWVYNELRVQLEERRGRRL  
15 RLCLEERDWPGLKTFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRLLDRKDVVVLVILRPAAYRSR  
YVRLRQLRCRQSVLLWPHQPSGQGSFWANLGIALTRDNRFYNRNFCRGPTTAE

## SEQ ID NO:10 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLTLPALPCELQPHGQVDCNWLFLKSVPHFSAAGAPRANVTSLSLISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTEIPNTFLAVPTLEELNLSYNGITTVPALPSSSLVLSLS  
20 HTSILVLGPTHFTGLHALRFLYMDGNCYMNPCCRALEVAPGALLGLGNLTHLSLKYNNTLEVPRLPPSLDTLL  
LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSISLYKLEK  
DWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNHYHKKVSFAHLHLASSFGSLVSLEKLDMHGIF  
RSLTNITLQSLTRLPLKQLSLHLQNLFINQAQLSIFGAFPSLLFVLDLSDNRISGAATPAAALGEVDSRVEVWRLPR  
25 GLAPGPLDAVSSKDFMPSCNLFNLTDLNRNLTITQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD  
LSHNKL DLYHGRSFTLPLQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSRLYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLNLPKSLRQLRLRDNNLAFFNWSSTVLP  
RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIPGFFVRATRLIELNLSANALKTVDPSWFGSLAGTL  
KILDVSANPLHCACGAAFVDFLLERQEA VPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETSLDCFG  
30

## SEQ ID NO:11 (Bovine TLR9)

gggaagtgggcgccaagcatccttcctgcagctgcctcccaacctgcccgcagacctctggagaagccgcat  
tccctgtcactgggcccctactgtgccccgcaccccccttctcctcctggtgcaggcgccgactggcagcgccc  
tgcccgaggcgccctgcctgccttctgcctgtgagctccagccccatggtcaggtggactgcaactggctgt  
35 tctgaagtctgtgcccgcacttttcggctggagcccccgcccaatgtcaccagcctctccttaactctccaacc  
gcatccaccactgtcatgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtggactgcc  
cgccggcgccgctcagccccatgcacttccccctgccgtatgaccatcgagcccaacaccttccctggctgtgcca  
ccctggaggagctgaacctgagctacaacggcatcacgacctgcctgcccagttccctcgtgtccctgt  
cgctgagccacaccagcatcctggtgctaggccccaccacttcacccggcctgcacgcccctgcgctttctgtaca  
40 tggacggcaactgctactacatgaaccctgcccggggccctggaggtggccccaggcgccctcctcgccctgg  
gcaacctcagcactgtcgctcaagtacaacaacctcacggaggtgccccggcgctgccccccagcctggaca  
ccctgtgctgtcctacaaccacattgtcaccctggcaccggaggacctggccaacctgactgcccctgcgctgc  
ttgacgtgggtgggaactgcgcgcgtgcgaccatgcccgaacccctgcagggagtgeccaaagaacttccca  
agctgcaccttgacaccttcagtcacctgagccgctcgaaggcctggtgtgaaggacagttctctctacaac  
45 tagagaaagattggttccgcgccctgggagggctccaagtgtcgacctgagtgaacttctctatgactaca  
tcaccaagaccacctcttcaacgacctgacctgagctgcgagactcaacctgtccttcaattaccacaagaagg  
tgtccttcgcccacctgcacctagcgtcctcctttgggagctctggtgtccctggagaagctggacatgcacggca  
tcttcttcgctccctcaccacatcacgctccagtcgctgacccggctgcccagctccagagctgtcatctgc  
agctgaacttcatcaaccaggcccagctcagcatctttgggccttcccagcctgtccttctgagacctgtcgg  
50 acaacgcatcagcgagcgcgacgcagcgccgctggggagggtggacagcaggggtggagctgtggcgat  
tgcccaggggctcgtccaggccgctggacgcgctcagctcaaaggacttcatgccaagctgcaacctcaact  
tcaccttgacctgtcacggaacaacctggtgacaatccagcaagagatgtttaccgcctctcccgcctccagt  
gcctgcgctgagccacaacagcatctcgaggcggttaatggctcccagttcgtgcgctgaccagcctgcgag

- 14 -

tgctcgacctgtcccacaacaagctggacctgtaccatggcgctcattcacggagctgcccagctggaggcac  
tggacctcagctacaacagccagcccttcagcatgcaggcgctggggccacaacctcagcttcgtggccagctgc  
cctccctgcgctacctcagccttgccgacaatggcatccacagccgctgtcacagaagctcagcagcgctcgt  
tgcgcgcccctggacttcagcggcaactccctgagccagatgtggggccgagggagacctctatctctgctttttca  
5 aaggcttgaggaaacctgggtccagctggacctgtccgagaacctctgcacaccctcctgcctcgtcacctggaca  
acctgcccagagcctgcccagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgaccg  
tcctgccccggctggaagccctggatctggcaggaaccagctgaaggccctgagcaacggcagcctgcccgcctg  
gcacccggctccagaagctggacgtgagcagcaacagcatcggttcgtgatccccggcttcttcgtccgcgcga  
ctcggtgatagagcttaacctcagcgccaatgcctgaagacagtggatccctcctgggttcggttcccttagcag  
10 ggacctgaaaatcctagacgtgagcgccaaccgctccactgcgcctgcccggcgccctttgtggacttctgc  
tggagagacaggaggccgtgcccgggctgtccaggcgctcacatgtggcagtcggggccagctccaggggccgca  
gcattctcacacaggacctgcgcctctgcctggatgagacctctccttggtactgctttggcctctcactgctaa  
tgggtggcgctgggctggcagtgcccatgctgcaccacctctgtggctgggacctctggtactgcttccacctgt  
gtctggcccatttgccccagcgccggcgccagcgggcgaggacacctgctctatgatgcgctcgtggtcttcg  
15 acaaggtgcagagtgcagtggtgattgggtgtacaacgagctccgcgtgcagctggaggagcgccggggcgcc  
ggcgctccgctctgcctggaggagcgagactggctccctggtaagacgctcttcgagaacctgtggcctcgg  
tctacagcagccgaagacctgttcgtgctggaccacagcgccgggtcagcgccctcctgcgcgcagcttcc  
tgctggccagcagcgctgttggaggaccgaaggacgtcgtagtgctggtgatcctgcgccccgcgcctatc  
gggtccgctacgtgcccgtgcgccagcgctctgcgccagagcgctcctcctctggccccaccagccagtgggc  
20 agggtagtttctgggccaacctgggcatagccctgaccaggggacaacctcacttctataaccggaacttctgcc  
ggggccccacgacagccgaatagcacagagtgcctcag

## SEQ ID NO:12 (Bovine TLR9)

atggggccctactgtgccccgcacccctttctctcctgggtgcaggcgccgagcactggcagcgccctggccgag  
25 ggcacctgctgccttctgcctgtgagctccagcccatgggtcaggtggactgcaactggctgttctgaag  
tctgtgccgacttttcggctggagcccccgggccaatgtcaccagcctctccttaatctccaaccgcatccac  
cacttgcatgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtggaaactgcccgcgcgc  
ggcctcagcccatgcacttccctgcgctatgacctcgagcccaacaccttctggctgtgcccacctggag  
30 gagctgaacctgagctacaacggcatcacgacctgcctgcctgccagttccctcgtgtccctgtcgtgagc  
cacaccagcatcctgggtgctaggccccaccacttcacggcctgcacgcctgcgcttctgtacatggacggc  
aactgctactacatgaacctcctgcccggggccctggaggtggccccaggcgccctcctcggcctgggcaacctc  
acgcacctgtcgtcaagtacaacaacctcacggaggtgccccgcgcgctgccccccagcctggacacctgctg  
ctgtcctacaaccacattgtcacctggcaccgaggaacctggccaacctgactgcctgcgctgcttgacgtg  
35 ggtgggaactgcccgcgtgcgacctgcccgaacctgcgggagtgccaaagaacttccccagctgcac  
cctgacaccttcagtcacctgagcgcctcgaaggctgggtgtgaaggacgttctctctacaacctagagaaa  
gattgggttcgcgcgctgggaggtcctcaagtgtcgacctgagtgagaacttctctatgactacatcaccaag  
accaccatcttcaacgacctgacctgagctgcgcagactcaacctgtccttcaattaccacaagaagggtgctctc  
ggccacctgcacctagcgtcctccttgggagctgtgtgctccctggagaagctggacatgcacggcatcttcttc  
cgtccctcaccacatcacgctccagtcgctgacctgggctgcccagctccagagctctgcatctgcagctgaac  
40 ttcataaccaggccagctcagcatcttggggccttcccagcctgctcttcgtggacctgtcggacaaccgc  
atcagcggagccgagcagccagcgccgcccctggggaggtggacagcagggaggatctggcgattgcccagg  
ggcctcgtccaggcccgctggacgcccgtcagctcaaaggacttcattgccaagctgcaacctcaacttcaccttg  
gacctgtcacggaacaacctgggtgacaatccagcaagagatgtttaccgcctctcccgcctccagtgccctgcg  
ctgagccacaacagcatctcgaggcggttaattggctcccagttcgtgcccgtgaccagcctgcgagtgctcgac  
45 ctgtcccacaacaagctggacctgtaccatgggcgtcattcacggagctgcccagctggaggcactggacctc  
agctacaacagccagcccttcagcatgcaggcgctggggccacaacctcagcttcgtggccagctgcccctcctg  
cgctacctcagccttgccgacaaatggcatccacagccgctgtcacagaagctcagcagcgccctgctgcgcgcc  
ctggacttcagcggcaactcctgagccagatgtggggcgaggagacctctatctctgcttttcaaaggcttg  
aggaacctgggtccagctggacctgtccgagaacctcagcaccctcctgcctcgtcacctggacaacctgccc  
50 aagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgacgctcctgccc  
cggtggaagccctggatctggcaggaaccagctgaaggccctgagcaacggcagcctgcccgcctggcatccg  
ctccagaagctggagctgagcagcaacagcatcggttcgtgatccccggcttcttcgtccgcgcgactcggtg  
atagagcttaacctcagcgccaatgcctgaagacagtggatccctcctgggttcggttcccttagcagggaacctg  
aaaatcctagacgtgagcgccaacctgcctcagcgtgcggggcgcccttgggtgacttctgctggagaga  
55 caggaggcctgcccgggctgtccaggcgctcacatgtggcagtcggggccagctccaggggccgagcatctc  
acacaggacctgcgctctgcctggatgagacctctccttggtgactgcttggc

## SEQ ID NO:13 (Equine TLR9)

5 MGPCHGALQPLSLLVQAAMLAVALAQGTLPFPLPCELOPHGLVNCNWLFLKSVPHFSAAAPRDNVTSLSLLSNRI  
HHLHDSDFQAQLSNLQKLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL  
SRTNILQLDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTTPRSLPPSLEYL  
LLSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSLSLYQLN  
PRWFRGLGNLTVDLSENFLYDCITTKTAFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSGSLLSLQELDMHGIF  
FRSLSQKTLQPLARLPMLQRLYLQMNFINQAQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS  
10 RDLTPGPLDTPSSEDFMPCKNLSFTLDLSRNNLVTVPQEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV  
LDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMRGVGHNLSFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL  
WALDFSGNSLSQMWAEGDLYLRFFQGLRSLIRLDLSQNRHLTLPLCTLGNLPKSLQLLRLRNNYLAFFNWSSTL  
LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRSNIIFVVPGFALATRLRELNLSANALRTEEPSWFGFLAG  
SLEVLDSANPLHACGAAFVDFLLQVQAAVPLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFGLSLLV  
VALGLAMPMLHHLGWDWYCFHLGLAWLPRRGWQRGADALSYPVFDKAQSAVADWVYNELRVRLEERRGR  
15 ALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDQVSGLLRASFLLAQQRLEDRKDVVVLVILSPDARR  
SRYVRLRQLRCRQSVLFWPHQPSGQRSFWAQLGMALTRDNRHFYNQNFRCRGPTMAE

## SEQ ID NO:14 (Equine TLR9)

20 MGPCHGALQPLSLLVQAAMLAVALAQGTLPFPLPCELOPHGLVNCNWLFLKSVPHFSAAAPRDNVTSLSLLSNRI  
HHLHDSDFQAQLSNLQKLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL  
SRTNILQLDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTTPRSLPPSLEYL  
LLSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSLSLYQLN  
PRWFRGLGNLTVDLSENFLYDCITTKTAFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSGSLLSLQELDMHGIF  
FRSLSQKTLQPLARLPMLQRLYLQMNFINQAQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS  
25 RDLTPGPLDTPSSEDFMPCKNLSFTLDLSRNNLVTVPQEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV  
LDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMRGVGHNLSFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL  
WALDFSGNSLSQMWAEGDLYLRFFQGLRSLIRLDLSQNRHLTLPLCTLGNLPKSLQLLRLRNNYLAFFNWSSTL  
LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRSNIIFVVPGFALATRLRELNLSANALRTEEPSWFGFLAG  
SLEVLDSANPLHACGAAFVDFLLQVQAAVPLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFG

## SEQ ID NO:15 (Equine TLR9)

ctctgttctctgagctgttgccgctgaaggactgagcagacaaagcatcctcctctgcagctgctgccagtg  
tgccagctggaccctctggatcatctcccactcctgtcatgggccccttgccatggtgcccctgcagccctgtct  
ctcctggtgcaggcgccatgctggcctggtcttgcccaggcaccctgcctcctctcctgcccctgtgagctc  
35 cagcccccagcgctggtgaactgcaactgctgttcttgaaagtcctgcccacttctcagcagcagcagccgg  
gacaatgtcaccagcttctccttgcctctccaaaccgcatccaccactccagactccgactttgcccactgtcc  
aacctgcagaaactcaacctcaaatggaactgcccggcagccggcctcagccccatgcacttcccctgccacatg  
accatcagaccccaacttctcctggtgtacccaccctggaggagctgaacctgagctacaacggcatcacgact  
gtgctgcccctgcccagctccctcgtgtccctgatcctgagccgcaccaacatcctgcagctagacccaccagc  
40 ctcacgggctgcatgcccctgcgcttctctatacatggatggcaactgctactacaagaaccttgccggcgccg  
ctggagggtggcccccaggcgccctccttgccctgggcaacctcaccacactgtcactcaagtacaacaacctcaca  
acgggtgcccgcagcctgcccctagcctggagtacctgctgtgtcctacaaccacattgtcaccctggcacct  
gaggacctggccaactcgtactgcccctgcgtgtgctcgatgtgggtggaactgcccgcgctgtgacctgcacgc  
aaccctgcgtggagtggccacataaattccccagctgcactccgacaccttcagccacctaaagccgctagaa  
45 ggccctgctgtgaaggatagttctctctaccagctgaacccagatggttccgtggcctgggcaacctcacagt  
ctcgacctgagtgagaacttctctacgactgcatcaccaaaaccaaggcattccagggcctggccagctgcga  
agactcaacttgccttcaattaccataagaaggtgtccttcgcccacctgacgctggcaccctccttcgggagc  
ctgctctccctgcaggaaactggacatgcatggcatcttctccgctcactcagccagaagacgctccagccactg  
gcccgcctgcccagctccagcgtctgtatctgcagatgaacttcataaccaggcccagctcgccatcttcaag  
50 gacttccctggtctgcgctacatagacctgtcagacaaccgcatcagtgaggctgtggagccggtggccaccaca  
ggggagggtgagtggtgggaagaaggtctggctgacatccaggacactcactccaggcccactggacccccagc  
tctgaggacttcatgccaagctgcaagaacctcagcttcaccttgacactgtcacggaacaacctggtaacagtc  
cagccagagatgtttgccagctctcgccgctccagtgccctgcgctgagccacaacagcatctcgcaggcggtc

- 16 -

aatggctcacagttcgtgccactgaccagcctgcagggtgctggacctgtcccataacaaactggacctgtaccat  
 gggcgctcgtttacggagctgccgcgactggaggccctggacctcagctacaacagccagcccttcagcatgcgg  
 ggtgtgggcccacaacctcagctttgtggccagctgccaccctgcgctacctcagcctggcacacaatggcatc  
 cacagccgtgtgtcccagcagctctgcagcacctcgctgtggggccctggacttcagcggcaattccctgagccag  
 5 atgtgggctgagggagacctctatctccgcttcttccaaggcctgagaagcctaattccggctagacctgtcccag  
 aatcgtctgcataccctcctgccatgcaccctgggcaacctccccaaagagcttgacgctgtcgcttccgtaac  
 aattacctggccttcttcaattggagcagcctgacctcctgcccacctggaaacctggacctggctggaaac  
 cagctgaaggctctgagcaatggcagcctgccttctggcaccagctccagaggctggacgtcagcaggaacagc  
 atcatcttcgtgggtccctggcttcttctgtctggccacgaggctgcgagagctcaacctcagtggcaacgcctc  
 10 aggcagagaggacccctcctgggttgggttctctagcaggtcccttgaagtcttagatgtgagcgccaacctctg  
 cactgcgcctgtggggcagccttctgtgacttctgctgcagggttcaggctgcctgtgctggctgtgccagccgc  
 gtcaagtgtggcagtcggggcagctccagggccgcagcatcttcgcacaagacctgcgcctctgctggacaag  
 tccctctcctgggactgttttgggtctctcattgctgggttgtggccctgggctggccatgcctatgttgaccac  
 ctctgcggtgggacctctggtactgcttccacctgggctggcctggctgccccgggggggtggcagcggggc  
 15 gcggtgcctgagctatgatgccttctgtggtcttcgacaaggcacagagcgcagtgggcgcactgggtgtacaat  
 gaactgcgggtgcggctagaggagcgcgctgggcccgcggcgctccgctgtgtctggaggagcgtgactggcta  
 cctggcaagacgctgttcgaaaacctgtggcctcagctctacagcagccgcaagatgctgttctgtgctggccac  
 acggaccaggtcagtgccctcttgcgtgccagcttctgctggcccagcagcgtctgctggaggaccgcaaggac  
 gttgtggtgctggtaactctgagccctgacgcccgcgcttcccgctacgtgcggtgcgccagcgcctctgccc  
 20 cagagtgtcctctctggccccaccagcctagtggccagcgcagcttctggggccagctaggcatggccctgacc  
 agggacaaccgcccacttctataaccagaacttctgccccggggccgacgatggctgagtagcacagagtgcagcc  
 tggcatgtacaacccccagccctgaccttgccctctgacctatgatgcccagctctgctcactctgtgacgccc  
 tgctctgctccgcccacctcacccttggcatacagcaggcactcaataaatgcccactggcaggccaaacagcca  
 aaaaaaaaaaaaaaaaaa

25

## SEQ ID NO:16 (Equine TLR9)

atgggccccttgccatgggtgccttcgagccctgtctctcctgggtgcaggcgggccatgctggccgtggctctggcc  
 caaggcaccttgccctcccttctgcccgtgtgagctccagccccacggcctgggtgaactgcaactggctgttccctg  
 aagtccgtgccccacttctcagcagcagcaccgccgggacaatgtcaccagccttctctgtctccaaccgcac  
 30 caccacctccagactccgactttgcccactgtccaacctgcagaaactcaacctcaaatgggaactgcccggca  
 gccggcctcagccccatgcacttccctgcccacatgacctcagagcccaacttctcctggctgtaccaccctg  
 gaggagctgaacctgagctacaacggcatcacgactgtgcctgcccctgccagctccctcgtgtccctgatcctg  
 agccgcaccaacatcctgcagctagaccccaccagcctcacgggctgcagcctgcccctgcgcttccctatacatggat  
 ggcaactgtactacaagaacctcgcggggggcctggagggtggcccaggcgccctccttggcctgggcaac  
 35 ctaccccacctgtcactcaagtacaacaacctcacacgggtgccccgcagcctgccccctaggctggagtacctg  
 ctgttctctacaaccacattgtcacccctggcacctgaggacctggccaactctgactgcccctgcgtgtgctcgat  
 gtgggtggaaactgcccgcgctgtgacctgcacgcaacctcgtgagggtggccacataaattccccagctg  
 cactccgacaccttcagccacctaaagcgcctagaaggcctcgtgtgaaggatagttctctctaccagctgaac  
 cccagatggttccgtggcctggcaacctcacagtgtcgacctgagtgagaacttccctctacgactgcacacc  
 40 aaaaccaaggcattccagggtcctggcccagctgcgaagactcaacttgccttcaattaccataagaagggtgtcc  
 ttcgcccacctgacgtggcaccctccttcgggagcctgctctcctgcaggaactggacatgcattggcatcttc  
 tccgctcactcagccagaagacgctccagccactggccgcctgcccctgctccagcgtctgtatctgcagatg  
 aacttcatcaaccaggcccagctcggcatcttcaaggacttccctggctcgcgtacatagacctgtcagacaac  
 cgcacagtgaggctgtggagccggtggccaccacaggggaggtggatgggtgggaagaaggctcctggctgacatcc  
 45 agggacctcactccaggcccactggacacccccagctctgaggacttcatgccaagctgcaagaacctcagcttc  
 accttggacctgtcacggaacaacctggtaacagtcacagccagagatgtttgcccagctctcgcgcctccagtg  
 ctgcccctgagccacaacagcatctcgcaggcggcctcaatggctcacagttcgtgcccactgaccagcctgcagggtg  
 ctggacctgtcccataacaaactggacctgtaccatgggcgctcgtttacggagctgcccgcgactggaggccctg  
 gacctcagctacaacagccagcccttcagcatgcggggtgtgggcccacaacctcagcttctgtggcccagctgccc  
 50 acctgcgctacctcagcctggcacacaactgcacagcgtgtgtcccagcagctctgcagacctcgtg  
 tgggcccctggacttcagcggcaattccctgagccagatgtgggctgaggagacctctatctccgcttcttccaa  
 ggccctgagaagcctaattccggctagacctgtcccagaatcgtctgcataacctcctgccatgcacctgggcaac  
 ctccccaaagagcttgacgtgtgctgcttccgtaacaattacctggccttcttcaattggagcagcctgacctc  
 ctgcccacacctggaaacctggacctgggtggaaaccagctgaaggctctgagcaatggcagcctgccttctggc  
 55 accagctccagaggctggacgtcagcaggaacagcatcatctcgtggtccctggcttcttctgctctggccacg  
 aggtgcgagagctcaacctcagtgccaacgcctcaggacagaggagccctcctgggttgggttctctagcaggc  
 tcccttgaagtcttagatgtgagcgccaacctctgcactgcgcctgtggggcagccttctgtggaactctcgtgctg

- 17 -

cagggttcaggctgccgtgcctggtctgccagccgcgtcaagtgtggcagtcggggccagctccaggggccgcagc  
atcttcgcacaagacctgcgcctctgcctggacaagtcctctcctgggactgttttgg

## SEQ ID NO:17 (Ovine TLR9)

5 MGPYCAPHPLSLLVQAAALAAALAQGTLPAPFLPCELQPRGKVCNWLFLKSVPFRFSAGAPRANVTSLSLISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVLSLS  
RTSILVLGPTHFTGLHALRFLYMDGNCYKNPCQQAQAVEVAPGALLGLGNLTHLSLKYNNTLEVPRLPPLSLDTLL  
LSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDFTSHLSRLEGLVLKDSLSLYKLEK  
10 DWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTLQRLRLNLSFNHYHKKVSFAHLQLAPSFGGLVLSLEKLDMHGIF  
RSLTNTTLRPLTQLPKLQSLSLQLNFINQAELSIFGAFPSLLFVLDSDNRISGAARPVAALGEVDSGVEVWRWR  
GLAPGPLAAVSAKDFMPSCNLTLDLSRNNLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRLRVLD  
LSYNKLDLYHGRSFTTELPQLEALDLSYNSQPFMSQGVGHNLFSVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLDNLPKSLRQLRLRDNNLAFNWSSTVLP  
15 QLEALDLAGNQLKALSNGSLPPGTRQLQKLDVSSNSIGFVTPGFFVLNRLKELNLSANALKTVDPFWFGRLTETL  
NILDVSPANLPHCACGAADFVDFLEMQAAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETSLDCFGFSLLMVA  
LGLAVPMLHHLGWDLDWYCFHLCLAHLPRLRRRQRGEDTLLYDAFVVFDKAQSAVADWVYNELRVQLEERRGRRL  
RLCLEERDWLPGKTLFENLWASVYSRKTMFVLDHTDRVSGLLRASFLLAQQRLLLEDKDVVVLVILRPAAYRSR  
YVRLRQLRCRQSVLLWPHQPSGQGSFWANLGMALTRDNRHFYNRNFCRGPTTAE

## 20 SEQ ID NO:18 (Ovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAQGTLPAPFLPCELQPRGKVCNWLFLKSVPFRFSAGAPRANVTSLSLISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVLSLS  
RTSILVLGPTHFTGLHALRFLYMDGNCYKNPCQQAQAVEVAPGALLGLGNLTHLSLKYNNTLEVPRLPPLSLDTLL  
LSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDFTSHLSRLEGLVLKDSLSLYKLEK  
25 DWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTLQRLRLNLSFNHYHKKVSFAHLQLAPSFGGLVLSLEKLDMHGIF  
RSLTNTTLRPLTQLPKLQSLSLQLNFINQAELSIFGAFPSLLFVLDSDNRISGAARPVAALGEVDSGVEVWRWR  
GLAPGPLAAVSAKDFMPSCNLTLDLSRNNLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRLRVLD  
LSYNKLDLYHGRSFTTELPQLEALDLSYNSQPFMSQGVGHNLFSVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLDNLPKSLRQLRLRDNNLAFNWSSTVLP  
30 QLEALDLAGNQLKALSNGSLPPGTRQLQKLDVSSNSIGFVTPGFFVLNRLKELNLSANALKTVDPFWFGRLTETL  
NILDVSPANLPHCACGAADFVDFLEMQAAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETSLDCFG

## SEQ ID NO:19 (Ovine TLR9)

gtcggcacgggaagtgcagcgccaagcatccttccctgcagctgcgcgccaacttgcgcgccaagacctctggaga  
35 agccgcattccctgccatggggccctactgtgcccgcaccccttctctcctggtgcaggcgccgctggc  
agcagccctggccaggccacctgctgccttccctgcccgtgagctccagcccggggtaaggtaactgcaa  
ctggctgttctgaagtctgtgcccgcgttttcggccggagcccccgggccaatgtcaccagcctctcctaat  
ctccaaccgcattccaccacttgacgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagt  
gaactgcccgcggccggcctcagcccatgcacttccctgcccgcagatgaccatcgagcccaacaccttccctggc  
40 tgtgcccacctggaggagctgaacctgagctacaatggcatcacgaccgtgctgcccgtgcccagttctctcgt  
atccctgtcgtgagccgcaccagcatcctggtgctaggccccaccacttcaccggcctgcagccctgcgctt  
tctgtacatggacggcaactgctactataagaacccctgccagcaggccgtggagtgcccccaggcgccctcct  
tggcctgggcaacctcacgcacctgtcgctcaagtacaacaacctcacggaggtgccccgcgctgccccccag  
cctggacacctgctgctgtcctacaaccacatcatcacctggcaccgcaggacctggccaatctgactgcctt  
45 gcgtgtgcttgatgtggcggggaactgccgcgctgcgaccacgcccgaaccttcagggagtgcccaaagaa  
cttccccaaagtgcacctgacaccttcagccacctgagccgctcgaaggcctggtgttgaggacagttctct  
ctacaaactagagaaagactggttccgcccgtggcgaggctccaagtgtcgacctgagtgagaacttctcta  
tgactacatcaccaagaccaccatcttcaggaacctgaccagctgcccagactcaacctgtccttaattacca  
caagaaggtgtccttcgcccacctgcaactggcaccctccttgggggctggtgtccctggagaagctggacat  
50 gcaaggcctcttctccgctccctcaccaaccacagctccggccgctgaccagctgcccagctccagagctc  
gagctgtcagctgaactcatcaaccagcgagctcagcatcttggggccttcccgagcctgctctcgtgga  
cctgtcggacaaccgcattcagcgagctgcgaggccggtggccgcccctggggaggtggacagcggggtggaagt  
ctggcggtggccaggggcctcgctccaggcccgctggccgcccgtcagcgcaaggacttcatgccaagctgcaa



- 18 -

cctcaacttcaccttggacctgtcacggaacaacctggtagcatccagcaggagatgtttaccgcctctccc  
cctccagtgcctgcgctgagccacaacagcatctcgcaggcggttaatggctegcagttcgtgccgtgacccg  
cctgcgagtgtcgacctgtcctacaacaagctggacctgtaccatgggcgctcgttcacggagctgccgcagct  
ggaggcactggacctcagctacaacagccagcccttcagcatgcaggggcgtgggccacaacctcagcttcgtggc  
5 ccagctgccgtccctgcgctacctcagccttgcgcacaacggcatccacagccgcgtgtcacagaagctcagcag  
cgctcgtgcgcgacctggacctcagcggcaactccctgagccagatgtggccgagggagacctctatctctg  
cttcttcaaaggcttgaggaacctgggtccagctggacctgtccaagaaccacctgcacacctcctgcctcgtca  
cctggataacctgcccagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcag  
cctgactgttctgccccagctggaagccctggatctggcgggaaaccagctgaaggccctgagcaacggcagcct  
10 gccacctggcaccggctccagaagctggacgtgagcagcaacagcatcggtttgtgaccttggttctttgt  
ccttgccaacggctgaaagagcttaacctcagcgccaacgcctgaagacagtggatcccttctggttcggctg  
cttaacagagacctgaatatcctagacgtgagcgccaacccgctccactgtgcctgcgggggcgcccttctgga  
cttctgctggagatgcaggggcgctgcctgggctgtccaggcgctcagctgtggcagtcggggccagctcca  
gggcgcagcatcttcgcacaggacctgcgcctctgcctggatgagacctctccttgactgcttggcttctc  
15 gctgctaagtgtggcgctgggctggcggtgccatgctgcaccacctctgtggctgggacctgtggtactgctt  
ccacctgttctggcccatcttgcggcgagcgggcgagcggggcgaggacacctgctctacagatgacctcgt  
ggcttctgacaaggcgagagtgagtgaggcgactgggtgtacaacagctccgcgtgcagctggaggagcgccg  
cgggcgccggcgctccgcctctgcctggaggagcgagactggctccctggcaagacgctcttcgagaacctgtg  
ggcctcggtctacagcagccgtaagacctgttctgctgagccacacggaccgggtcagtgccctcctgcgcgc  
20 cagcttctgctggccagcagcgctgttgaggagccgaaggatgtcgtggtgctggtgatcctgcgccccgc  
cgctaccgggtcccgctacgtgcggctgcgcagcgctctgcgcagagcgctcctccttgccccaccagcc  
cagtgggcagggtagcttctgggccaacctgggcatggccctgaccagggacaaccgccacttctataaccggaa  
cttctgcgggggccccacgacagccgaatagcacagagtgaactgcccag

## 25 SEQ ID NO:20 (Ovine TLR9)

atggggccctactgtgccccgaccccccttctctcctggtagcaggcgggcgctggcagcagccctggcccag  
ggcaccctgcctgccttctgcctgtgagctccagccccgggtaagggtgaactgcaactggctgttctgaag  
tctgtgccgcgcttttgcggcgagccccccgggccaatgtcaccagcctctccttaatctcaaccgcacccac  
cacttgcacgactctgacttctcaccctgtccaacctgcgggtcctcaacctcaagtggaaactgccgcgggccc  
30 ggctcagccccatgcacttccctgcgcgatgacctcagagcccaacaccttcttggtgtgcccacctggag  
gagctgaacctgagctacaatggcatcacgacctgcctgcctgccagttctctcgtatccctgtcgtgagc  
cgcaccagcatcctgggtgctaggccccaccacttcacgggctgcagccctgcgcttctctgtacatggacggc  
aactgctactataagaaccttgcagcaggccgtggagggtggcccgagcgccctccttgccctgggcaacctc  
acgcacctgtcgtcaagtacaacaacctcacggaggtgccccgcgcctgcccccaagcctggacacctgtctg  
35 ctgtcctacaaccacatcatcaccctggcaccgaggacctggccaatctgactgccctgcgtgtgcttgatgtg  
ggcggaactgcgcgcgctgcgaccacgcccgaacctgcaggagtgcccaagaacttccccagctgcac  
cctgacaccttcagccacctgagcgcctcgaaggcctgggtgttgaaggacagttctctctacaaactagagaaa  
gactggttcggcgccctgggcaaggctccaagtgtcgacctgagtgagaacttctctatgactacatcaccaag  
accaccatcttcaggaacctgacccagctgcgcagactcaacctgtccttcaattaccacaagaagggtgtcctc  
40 gccacctgcaactggcaccctccttgggggctggtgtccctggagaagctggacatgcagggcatcttcttc  
cgctccctcaccacaccacgctccggcgctgaccagctgcccagctccagagctgagctctgcagctgaac  
ttcatcaaccaggccgagctcagcatcttggggccttcccagcctgctcttcgtggacctgtcggacaaccgc  
atcagcggagctgcgaggccggtggcgccctcggggaggtggacagcgggggtggaagtctggcggtggccagg  
ggcctcgtccaggcccgctggccgcgctcagcgcaaggacttcatgccaagctgcaacctcaacttcaccttg  
45 gacctgtcaggaacaacctggtgacgatccagcaggagatgtttaccgcctctcccgcctccagtgcctgcgc  
ctgagccacaacagcatctcgcaggcggttaatggctcgcagttcgtgccgctgaccgcctgcgagtgctgcac  
ctgtcctacaacaagctggacctgtaccatggcgctcgttcacggagctgccgcagctggaggcactggacctc  
agctacaacagccagcccttcagcatgcaggcgctggggccacaacctcagcttctggtggccagctgacctcctg  
cgctacctcagcttgcgcacaacggcatccacagcgctgtcacagaagctcagcagcgctcgtcgtgcgcgc  
50 ctggacttcagcggcaactcctgagccagatgtggcgaggagacctctatctctgtcttctcaaaggcttg  
aggaacctgggtccagctggacctgtccaagaaccacctgcacacctcctgcctcgtcacctggataacctgccc  
aagagcctgcggcagctgctctccgggacaataacctggccttcttcaactggagcagcctgactgttctgccc  
cagctggaagccctggatctggcgggaaaccagctgaaggccctgagcaacggcagcctgccacctggcaccgg  
ctccagaagctggacgtgagcagcaacagcatcggtttgtgaccttggttcttctgcttgcgaaccggctg  
55 aaagagcttaacctcagcgccaacgcctgaagacagtggatcccttctggttcggtcgttaacagagacctg  
aatatcctagacgtgagcgccaaccgctccactgtgcctgcggggcgcccttctggtgacttctgctggagatg



- 19 -

caggcgccgtgcctgggctgtccaggcgcggtcacgtgtggcagtcggggccagctccaggggccgcagcatcttc  
gcacaggacctgcgcctctgcctggatgagacctctccttggaactgctttggc

Complete nucleotide and amino acid sequences for canine and feline TLR9 are  
publicly available. For example, an amino acid sequence for canine TLR9 is available as  
GenBank accession number BAC65192 and its corresponding nucleotide sequence is  
available as GenBank accession number AB104899. An amino acid sequence for feline  
TLR9 is available as GenBank accession number AAN15751 and its corresponding  
nucleotide sequence is available as GenBank accession number AY137581.

Complete nucleotide and amino acid sequences for canine and feline TLR9 were also  
determined independently from those available from public databases.

An amino acid sequence of canine TLR9 is provided as SEQ ID NO:21. Based on  
comparison with known amino acid sequences of human and murine TLR9, it appears that  
SEQ ID NO:21 includes sequence for at least a majority of the extracellular domain, all of the  
transmembrane domain, and at least a portion of the intracellular domain of canine TLR9  
(See Figure 1). Amino acids numbered 1-822 of SEQ ID NO:21 are presumptively  
extracellular domain and correspond to SEQ ID NO:22. SEQ ID NO:23 is a nucleotide  
sequence of canine TLR9 cDNA having an open reading frame corresponding to nucleotides  
91-3186. SEQ ID NO:24 is a nucleotide sequence of canine cDNA encoding amino acids 1-  
822 of SEQ ID NO:21.

An amino acid sequence of feline TLR9 is provided as SEQ ID NO:25. Based on  
comparison with known amino acid sequences of human and murine TLR9, it appears that  
SEQ ID NO:25 includes sequence for at least a majority of the extracellular domain, all of the  
transmembrane domain, and at least a portion of the intracellular domain of feline TLR9 (See  
Figure 1). Amino acids numbered 1-820 of SEQ ID NO:25 are presumptively extracellular  
domain and correspond to SEQ ID NO:26. SEQ ID NO:27 is a nucleotide sequence of feline  
TLR9 cDNA having an open reading frame corresponding to nucleotides 87-3179. SEQ ID  
NO:28 is a nucleotide sequence of feline cDNA encoding amino acids 1-820 of SEQ ID  
NO:25.

#### SEQ ID NO:21 (Canine TLR9)

MGPCRGALHPLSLLVQAAALALALAQGTLPALFLPCELQPHGLVNCNWLFLKSVPRFSAAAPRGNVTLSLSLYSNRI  
HHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCHMTIEPNTFLAVPTLEDLNLNSYNSITTVPALPSSLVLSLSL  
SRTNIVLDPATLAGLYALRFLFDGNCYYKNPCQALQVAPGALLGLGNLTHLSLKYNNLTVVPRGLPPSLEYL

- 20 -

LLSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKGFQQLHPNTFGHLSHLEGLVLRDSSLYSLD  
 PRWFHGLGNLMVLDLSENFLYDCITKTKAFYGLARLRLNLSFNHKKVSAHLHLASSFGSLLSLQELDIHGIF  
 FRSLSKTTLQSLAHLPLQLRLHLQNLFIQAQLSIFGAFPLRYVDLSDNRISGAAPAAATGEVEADCGERVWP  
 QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL  
 5 RVLDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMRGVGHNLSFVAQLPALRYLSLAHNGIHSRVSQQLRSA  
 SLRALDFSGNTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNLRLHTLLPRNLDNLPKSLRLLRLRDNYLAFFNWSSL  
 ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVPSPFALAVRLRELNLSANALKTVEPSWFGSL  
 AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWSVCFSL  
 LAVALSLAVPMLHQLCGWDLWYCFHLCLAWLPRRGRRGVDALAYDAFVVDKAQSSVADWVYNELRVQLEERRG  
 10 RRALRLCLEERDWPVKTLFENLWASVYSSRKTFLVLAARTDRVSGLLRASFLLAQQRLLDRKDVVVLVILCPDA  
 HRSRYVRLRQLRCRQSVLLWPHQPSGQRSFWAQLGTALTRDNHRHFNQNFRCRGPPTA

## SEQ ID NO:22 (Canine TLR9)

MGPCRGALHPLSLLVQAAALALALAQGTLPAPLPCELQPHGLVNCNWLFLKSVPRFSAAAPRGNVTSLSLYSNRI  
 15 HHLHDYDFVHVLRLRLNWKNCPPASLSPMHFPCMTIEPNTFLAVPTLEDNLNSYNSITTVPALPSSLVSLSL  
 SRTNIVLDPATLAGLYALRFLFDGNCYKNPCQQALQVAPGALLGLNLTHLSLKYNNTLVPRGLPPSLEYL  
 LLSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKGFQQLHPNTFGHLSHLEGLVLRDSSLYSLD  
 PRWFHGLGNLMVLDLSENFLYDCITKTKAFYGLARLRLNLSFNHKKVSAHLHLASSFGSLLSLQELDIHGIF  
 20 FRSLSKTTLQSLAHLPLQLRLHLQNLFIQAQLSIFGAFPLRYVDLSDNRISGAAPAAATGEVEADCGERVWP  
 QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL  
 RVLDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMRGVGHNLSFVAQLPALRYLSLAHNGIHSRVSQQLRSA  
 SLRALDFSGNTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNLRLHTLLPRNLDNLPKSLRLLRLRDNYLAFFNWSSL  
 ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVPSPFALAVRLRELNLSANALKTVEPSWFGSL  
 25 AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWSVCF

## SEQ ID NO:23 (Canine TLR9)

aggaaggggctgtgagctccaagcatcctttcctgcagctgctgcccagcctgccagccagaccctctggagaag  
 cccccgctccctgtcatgggcccctgccgtggcgccctgcacccctgtctctcctgggtgcaggtgccgcgcta  
 gccctggcctggcccagggcaccctgacctcctcctgcctgtgagctccagcccatggcctgggtgaactgc  
 30 aactggctgttccctcaagtcctgtgccccgcttctcggcagctgcaccccgcggtaacgtaccagcctttccttg  
 tactccaaccgcatccaccacctccatgactatgactttgtccacttcgtccacctgcccgtctcaatctcaag  
 tggaaactgcccgcggccagcctcagcccatgacactttcctgtcacatgaccattgagcccaacaccttcttg  
 gctgtgcccaccctagaggacctgaatctgagctataacagcatcacgactgtgcccgcctgccaggttcgctt  
 gtgtccctgtccctgagccgcaccaacatcctgggtgctggaccctgccaccctggcaggcctttatgccctgctg  
 35 ttccctgttccctggatggcaactgctactacaagaacccctgccagcaggccctgcaggtggccccaggtgccctc  
 ctgggctgggcaacctcacacacctgtcactcaagtacaacaacctcacctgggtgccgcggggcctgcccccc  
 agcctggagtagctgtccttctcctacaaccacatcatcaccctggcactgaggacctggccaatctgactgcc  
 ctgcgtgtcctcgatgtgggtgggaactgtcgccgctgtgaccatgccgtaaccctgcaggagtgcccaag  
 ggcttccccagctgcaccccaacaccttcggccacctgagccacctcgaaggcctgggtgtgagggacagctct  
 40 ctctacagcctggacccaggtggttccatggcctgggcaacctcatggtgctggacctgagtgagaacttcttg  
 tatgactgcatcaccaaaacaaagccttctacggcctggcccggtgcgcagactcaacctgtccttcaattat  
 cataagaaggtgtcctttgccacctgcatctggcatcctccttcgggagcctactgtccctgcaggagctggac  
 atacatggcatcttcttcgctcgctcagcaagaccagctccagtcgctggccacctgccatgctccagcgt  
 ctgcatctgcagttgaactttatcagccaggccagctcagcatcttcggcgcttccctggactgcggtacgtg  
 45 gacttgtcagacaaccgcatcagtgagctgcagagcccggtgccacaggggaggtagaggcagactgtggg  
 gagagagtctggccacagctccgggacctgtctggggccactgggcaccccggtcagaggccttcagtcg  
 agctgcaggacctcaacttcaccttggacctgtctcggaacaacctagtgactgttcagccggagatgtttgtc  
 cggctggcgccctccagtgctgggctgagccacaacagcatctcgaggcggtcaatggctcgagttcgtg  
 cctctgagcaacctgcgggtgctggacctgtccataacaagctggacctgtaccacgggcgctcgttcacggag  
 50 ctgcccgggctggaggccttggacctcagctacaacagccagccctcagcatgcggggcgtggggccacaatctc  
 agctttgtggcacagctgccagccctgctacctcagcctggcgcaaatggcatccacagccgcgtgtcccag  
 cagctccgcagcgcctcgctccgggcccctggacttcagtggaataaccctgagccagatgtgggcccaggaggag  
 ctctatctcgacttcttccaaggcctgagaagcctgggtcagctggacctgtcccagaatcgctgcataccctc  
 55 ctgccacgcaacctggacaacctccccaaagcctcgggctcctgcggctccgtgacaattacctgcttctctc  
 aactggagcagcctggccctcctaccaagctggaagccctggacctggcgggaaaccagctgaaggccctgagc

- 21 -

aatggcagcttgcccaacggcaccagctccagaggctggacctcagcggcaacagcatcggcttcgtgggtcccc  
 agcttttttgccttgccgtgaggttcgagagctcaacctcagcgccaacgccctcaagacggtggagccctcc  
 tggtttgggtccctggcgggtgcctgaaagtcttagacgtgaccgccaaccccttgcatcgttcggtgcgca  
 accttcgtggacttcttgctggaggtgcaggctgcggtgcccggcctgcctagccgtgtcaagtgcggcagcccg  
 5 ggccagctccaggccgcagcatcttcgcacaggacctgcgcctctgcctggacgaagcgtctcctgggtctgt.  
 ttcagcctctcgtgctggctgtggcctgagcctggctgtgcccattgctgcaccagctctgtggctgggacctc  
 tggtaactgcttccacctgtgcctggcctggctgccccggcgggggcgggggtgtggatgcctggcctat  
 gacgccttcgtgggtcttcgacaaggcgagagctcggtggcgactgggtgtacaatgagctgcgggtacagcta  
 gaggagcgccgtggggcgccggcgctacgcctgtgtctggaggaaactgactgggtaccggcggcaaacctcttc  
 10 gagaacctctgggctcagtttacagcagccgcaagacgtgtttgtgctggcccgacggacagagtcagcggc  
 ctctgctgacgcttctgctggcccaacagcgcctgctggaggaccgcaaggacgtcgtgggtgctggtgatc  
 ctgtgccccgacgcccacgctcccgtatgtgcggtgcgcccagcgcctctgcccagagtgctcctcctctgg  
 cccaccagccagtggtggccagcgagcttctggggccagctgggcacggccctgaccagggacaaccgccacttc  
 tacaaccagaacttctgccccggggccacagacgctgataggcagacagccagcaccttcgcgccccctacacc  
 15 ctgctgtctgtctgggatgcccagctgctggctctacaccgcccgtctgtctccccctacaccagccctggca  
 taaagcgaccgctcaataaatgctgctggtagac

## SEQ ID NO:24 (Canine TLR9)

atggggccctgcccgtggcgccctgcacccctgtctctcctgggtgcaggctgcccgcgtagccctggccctggcc  
 20 cagggcacccctgcctgccttccctgcctgtgagctccagccccatggcctgggtgaactgcaactggtctgttcctc  
 aagtccgtgccccgcttctcggcagctgcaccccgcggttaacgtcaccagccttctcctgtactccaaccgcatc  
 caccacctccatgactatgactttgtccacttcgtccacctgcccgtctcaatctcaagtggaaactgcccggcc  
 gccagcctcagccccatgcactttccctgtcaatgaccattgagcccaacaccttctgggtgtgcccacccta  
 gaggacctgaatctgagctataacagcatcacgactgtgcccgcctgcccagttcgttgtgtccctgtccctg  
 25 agccgcaccaacatccctgggtgctggacctgcccacctggcaggcctttatgcctgcgcttctctgttccctggat  
 ggcaactgtactacaagaacccctgcccagcaggccctgcagggtggccccaggtgcctcctgggctgggcaac.  
 ctcacacacctgtcactcaagtacaacaacctcacctgggtgcccggggcctgccccccagcctggagtaactg.  
 ctcttgtcctacaaccacatcatcacctggcacctgaggacctggccaatctgactgcccctgcgtgtcctcgat  
 gtgggtgggaactgtgcgcgtgtgaccatgcccgttaacccctgcaggagtgccccaagggttccccagctg  
 30 caccccaacaccttcggccacctgagccacctcgaaggcctgggtgttgaggagacagctctctctacagcctggac  
 ccaggtgggttccatggcctgggcaacctcatgggtgctggacctgagtgagaacttctgtatgactgcatcacc  
 aaaaccaaagccttctacggcctggcccggctgcgcagactcaacctgtccttcaattatcataagaagggtgtcc  
 tttgcccacctgcatctggcatctccttcgggagcctactgtccctgcaggagctggacatacatggcatcttc  
 ttccgctgcctcagcaagaccagctccagtcgctggcccacctgcccagctcagcgtctgcatctgcagttg  
 35 aactttatcagcccaggccagctcagcatcttcggcgcccttccctggactgcggtacgtggacttctcagacaac  
 cgcacagtgaggctgcagagcccgcggctgccacaggggaggttagaggcagactgtggggagagagctctggcca  
 cagtcccgggaccttgccttggggccactgggcacccccggctcagaggccttcatgcccagctgcaggacctc  
 aacttcaccttggaacctgtctcggaacaacctagtactgttcagccggagatgtttgtccggctggcgccctc  
 cagtgcctgggctgagccacaacagcatctcgcaggcggtcaatggctcgcagttcgtgcctctgagcaacctg  
 40 cgggtgctggacctgtcccataacaagctggacctgtaccacgggcgctcgttcacggagctgcccgggctggag  
 gccttggacctcagctacaacagccagccctcagcatgcggggcgtgggcccacaatctcagctttgtggcacag  
 ctgccagcctgcgctacctcagcctggcgcaacaatggcatccacagccgctgtcccagcagctccgcagcgc.  
 tcgctccgggcccctggacttcagtggaataacctgagccagatgtggggccgaggagacctctatctccgcttc  
 ttccaaggcctgagaagcctgggttcagctggacctgtcccagaatgcctgcataacctcctgccacgcaacctg  
 45 gacaacctccccaagagcctgcggctcctgcggctccgtgacaattacctggctttcttcaactggagcagcctg  
 gccctcctacccaagctggaagcctggacctggcgggaaaccagctgaaggccctgagcaatggcagcttgccc  
 aacggcacccagctccagaggctggacctcagcggcaacagcatcggcttcgtgggtcccagcttttttgcctg  
 gccgtgaggcttcagagctcaacctcagcgccaacgccctcaagacggtggagccctcctgggtttgggtccctg-  
 50 gcggtgcccgtgaaagtcttagacgtgaccgccaaccccttgcatcgttcggtgcggcgcaaccttcgtggacttc  
 ttgctggaggtgcaggctgcgggtgcccggcctgctagccgtgtcaagtgcggcagccgggagcctccagggc  
 cgcagcatcttcgcacaggacctgcgcctgctggacgaagcgtctcctgggtctgtttcagc

## SEQ ID NO:25 (Feline TLR9)

MGPCHGALHPLSLLVQAAALAVALAQGTLPALFLPCELQRHGLVNCDWLFLKSVPHFSAAAPRGNVTSLSLSYNSRI  
 55 HHLHDSDFVHLSSLRRLNLKWNCPASLSPMHFPCHMTIEPHTFLAVPTLEELNLSYNSITTPALPSSLSLSL

- 22 -

SRTNIIIVLDPANLAGLSLRFLELDGNCYYKNPCQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL  
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRCDHARNPCMECPKGFPHLHPDTFSLHNHLEGLVLKDSLSYLN  
 PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNHKKVSAHLHLAPSFGLSLSLQQLDMHGIF  
 FRSLSETTLRSLVHPLMLQSLHLQMNFINQAQLSIFGAFPLGRYVLDSDNRISGAMELAAATGEVDGGERVRLPS  
 5 GDALGPPGTPSSEGFMPGCKTLNFTLDLSRNNLVTIQPEMFARLSRLQCLLLSRNSISQAVNGSQFMPLTSLQV  
 LDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMSQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASL  
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNRLHTLLPRTLNDNLPKSLRLLRLRDNYLAFFNWSSSLV  
 LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVASSFFALATRLRELNLSANALKTVEPSWFGSLAG  
 10 TLKVLDVTGNPLHCACGAFAVDFLLEVQAAPVGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCLSLT  
 VALGLAVPMLHHLGWDLYCFHLCLAWLPRRGRRRGADALPYDAFVFDKAQSAVADVWYNELRVRLERERRRR  
 ALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQQLLEDKRDVVVLVILRPDAHR  
 SRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNQHFYNQNFRCGPPTAE

## SEQ ID NO:26 (Feline TLR9)

15 MGPCHGALHPLSLVQAAALAVALAQGTLPAPFLPCELQRHGLVNCDFLKSVPHFSAAPRGNVTSLSLYSNRI  
 HHLHDSDFVHLSSLRRLNLKWNCPASLSPMHFPCMTIEPHTFLAVPTLEELNLSYNSITVPALPSSLSVLSL  
 SRTNIIIVLDPANLAGLSLRFLELDGNCYYKNPCQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL  
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRCDHARNPCMECPKGFPHLHPDTFSLHNHLEGLVLKDSLSYLN  
 20 PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNHKKVSAHLHLAPSFGLSLSLQQLDMHGIF  
 FRSLSETTLRSLVHPLMLQSLHLQMNFINQAQLSIFGAFPLGRYVLDSDNRISGAMELAAATGEVDGGERVRLPS  
 GDALGPPGTPSSEGFMPGCKTLNFTLDLSRNNLVTIQPEMFARLSRLQCLLLSRNSISQAVNGSQFMPLTSLQV  
 LDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMSQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASL  
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNRLHTLLPRTLNDNLPKSLRLLRLRDNYLAFFNWSSSLV  
 LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVASSFFALATRLRELNLSANALKTVEPSWFGSLAG  
 25 TLKVLDVTGNPLHCACGAFAVDFLLEVQAAPVGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCLG

## SEQ ID NO:27 (Feline TLR9)

agggctctgcgagctccaggcattctctctctgccatcgctgcccagctctgccatccagaccctctggagaagcccc  
 cactccctgtcatgggccccctgccatggcgccccctgcacccccctgtctctcctgggtgcaggtgcgcgctggccg  
 30 tggccctggccagggcaccctgcctgcctttctgccctgtgagctccagcgccacggcctggatgaattgcgact  
 ggctgttccctcaagtcctgcctgccccacttctcgccggcagcgccccctggtaacgtcaccagccttccctgtact  
 ccaaccgcatccacacccctccagcactccgactttgtccacctgtccagcctgcggcgctctcaacctcaaatgga  
 actgccccccgcagcctcagccccatgcacttccctgtcacatgaccattgagccccacaccttccctggccg  
 tgccccacctggaggagctgaacctgagctacaacagcatcacgacagtaccgccccctgccaggttccctcgtgt  
 35 cctgtccttgagccgtaccaacatcctgggtgctggaccctgccaacctcgagggctgcactccctgcgcttct  
 tggtcctggatggcaactgctactacaagaaccttgcccgagggcctgcaggtggccccggcgccctccttg  
 gctgggcaaccttacgcacctgtcactcaagtacaacaacctcactgcggtgcccccgcgccctgccccccagcc  
 tggagtacctgctattgtctacaaccacatcatcaccctggcacctgaggacctggccaacctgaccgcctgc  
 gtgtgctcgatgtgggtgggaactgccgtcgctgtgaccacgcccgaacctgtatggagtgcaccaagggt  
 40 tcccgacctgcacctgacacctcagccacctgaâccacctcgaaggcctgggtgttgaggacagctctctct  
 acaacctgaacccagatgggtccatgccccgggcaacctcatggtgctggacctgagtgagaacttccatatg  
 actgcatcaccaaaaccacagccttccagggcctggcccagctgcgcagactcaacttgtcttcaattaccaca  
 agaaggtgtcctttgcccacctgcactgtggcgccctccttcgggagcctgctctccctgcagcagctggacatgc  
 atggcatcttctccgctcgctcagcgagaccagctccggctcgctgggtccacctgcccagctccagagctctgc  
 45 acctgcagatgaacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggacc  
 tgtcagacaaccgcataagtggagccatggagctggcgctgccacggggaggtggatgggtggggagagagctcc  
 ggctgccatctggggacctagctctggggccacggcgacccctagctccgagggttcatgctcaggctgcaaga  
 ccctcaacttcccttgacctgtcacggaacaacctagtgaacatccagccagagatgtttgcccggctctcgc  
 gcctccagtgctgctcctgagccgaacagcatctcgaggcagtcacaggtcaccaatttatgccgctgacca  
 50 gcctgcaggtgctggacctgtcccataacaagctggacctgtaccatggcgctctttcacggagctgccgcggc  
 tggaggccctggacctcagctacaacagccagcccttcagcatgcaggcgctgggtcacaacctcagcttctgtg  
 cacagctgcggccctgcgctatctcagcctggcgcaaacgacatccacagccgtgtgtcccagcagctctgca  
 ggcctcgtgcgggccttgacttcagcggcaatgccttgagccgagtggtggggcggaggagacctgtatctcc  
 acttctccgaggcctgaggagcctggctcgggtggatctgtccagaatcgctgcataacctcttgccacgca  
 55 cctggacaacctccccaaagagcctgcggctgctgcgctctccgtgacaatttatctggcttcttcaactggagca

- 23 -

gcctgggtcctcctccccaggctggaagccctggacctggcgggaaaccagctgaaggccctgagcaacggcagct  
 tgcctaattggaacccagctccagaggctggacctcagcagcaacagtatcagcttcgtggcctccagcttttttg  
 ctctggccaccaggctgagagctcaacctcagtgccaacgccctcaagacggaggagccctcctgggttcggtt  
 ctctagcgggacccctgaaagtcttagatgtgactggcaacccctgcactgcgcctgtggggcgcccttcgtgg  
 5 acttcttgcctggagggtgaggtgagctgagctgcccggcctgccaggccacgtcaagtgtggcagtcagggtcagctcc  
 agggccgcagcatctttgcgcaggatctgcgcctctgcctggatgaggccctctcctgggactgttttggcctct  
 cgctgctgaccgtggccctgggctggcctgcccagctgcaccacctctgtggctgggacctctggtactgct  
 tccacctgtgcctggcctggctgccccggcgggggcgggcgggggcgggatgcccctgacctacgatgcctttg  
 10 tggctctcgacaaggcacagagcgcggtggccgactgggtgtacaacagagctgcgggtacggctagaggagcgcc  
 gtggacgcccagcgctccgctgtgcctggaggaaactgactggctaccgggtaaaacgctctttgagaacctgt  
 gggcctcagtttacagcagccgcaagatgctgtttgtgctggcccacacagacagggtcagcgccctcttgcgcg  
 ccagctttctgctggcccagcagcgctgctggaggaccgcaaggacgttgggtgctgggtgatcctgcgccccg  
 acgcccacgctcccgcctatgtgcggctgcgccagcgctctgcgccagagcgctcctcctctggccccaccagc  
 ccagtgggccagcgagcttctggggccagctgggacggccctgaccagggaacaaccagcactctataaccaga  
 15 acttctgcggggggccacgacggcagagtgaccgcccagcaccccaagcctcctacaccttgctgtctgcctg  
 ggtgcccggg

## SEQ ID NO:28 (Feline TLR9)

atggggccctgcccagggcgcctgcacccctgtctcctcctgggtgcaggtgcgcgcctggccgtggccctggcc  
 20 cagggcacccctgcctgcctttctgcctgtgagctccagcgccacggcctgggtgaattgcgactggctgttcctc  
 aagtccgtgccccacttctcgccggcagcgcccggtggttaacgtcaccagcctttccctgtactccaaccgcatc  
 caccacctccaagactccgactttgtccacctgtccagcctgcccgtctcaacctcaaactggaactgccaccc  
 gccagcctcagccccatgcacttccctgtcacatgaccattgagccccacaccttccctggccgtgccacccctg  
 25 gaggagctgaacctgagctacaacagcatcacgacgtaccgcctgcccagttccctcgtgctccctgtccttg  
 agccgtaccaacatcctgggtgctggaccctgccaacctgcagggctgcactccctgcgccttctgttccctggat  
 ggcaactgctactacaagaacccctgcccgcaggccctgcaggtggccccggcgccctccttggcctgggcaac  
 cttacgcacctgtcactcaagtacaacaacctcactgcgggtgccccgcggcctgccccccagcctggagtacctg  
 ctattgtcctacaaccacatcatcaccctggcactgaggacctggccaacctgaccgcctgcgtgtgctcgat  
 30 gtgggtgggaactgcccgtgctgtgaccacgcccgaacccctgtatggagtggccaagggtctcccgacactg  
 caccctgacaccttcagccacctgaaccacctcgaaggcctgggtgtgaaggacagctctctctacaacctgaac  
 cccagatgggtccatgcccctgggcaacctcatggtgctggacctgagtgaagaacttccatatgactgcacacc  
 aaaaccacagccttccagggcctggcccagctgcgcagactcaacttgtctttcaattaccacaagaagggtgtcc  
 tttgcccacctgcactgcccgcctccttcgggagcctgctctccctgcagcagctggacatgcacatcttct  
 35 ttcgctcgtcagcgagaccagctccggctgctgggtccacctgcccagctgctccagagctgcacctgcagatg  
 aacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggaactgtcagacaac  
 cgcataagtggagccatggagctggcggtgcccagggggagggtggatgggtggggagagagtcoggtgcatct  
 ggggacctagctctggggccacggggcaccctagctccgagggttcatgccaggctgcaagacctcaacttc  
 accttggacctgtcacggaacaacctagtgaacaatccagccagagatgtttgcccggctctcgccctccagtg  
 40 ctgctcctgagccgcaacagcatctcgaggcagctcaacggctcacaatttatgccgctgaccagcctgcaggtg  
 ctggacctgtcccataacaagctggacctgtaccatgggcgctcttccagggagctgcccgggctggaggccctg  
 gacctcagctacaacagccagcccttcagcatgcaggcgctgggtcacaacctcagcttctgtggcacagctgccc  
 gccctgcgctatctcagcctggcgcaacaacgacatccacagccgtgtgtcccagcagctctgcagcgccctg  
 45 cgggcttggacttcagcggcaatgccttgagccggatgtgggagggagacctgtatctccacttcttccga  
 ggccctgaggagcctgggtccgggtggatctgtcccagaatgcctgcataacctcttgccacgcacctggacaac  
 ctccccagggctggaagccctggacctggcggaaccagctgaaggccctgagcaacggcagcttgccaatgga  
 acccagctccagaggctggacctcagcagcaacagtatcagcttctgtggcctccagctttttgtctggccacc  
 aggtgcgagagctcaacctcagtgccaacgccctcaagacgggtggagccctcctgggttcgggttctctagcggg  
 50 accctgaaagtcttagatgtgactggcaacccctgcactgcgcctgtggggcgccctcgtggacttcttgcgtg  
 gagggtgaggctgagctgcccggcctgcccaggccagctcaagtgtggcagtcagggtcagctccaggggccgcagc  
 atctttgcgcaggatctgcgcctctgcctggatgaggccctctcctgggactgttttggc

Complete nucleotide and amino acid sequences for murine and human TLR9 are publicly available. For example, an amino acid sequence of murine TLR9 is available as

- 24 -

GenBank accession no. AAK29625, provided as SEQ ID NO:29. Amino acids numbered 1-821 of SEQ ID NO:29 presumptively include the entire extracellular domain and correspond to SEQ ID NO:30. SEQ ID NO:31 corresponds to GenBank accession number AF348140, which is a nucleotide sequence of murine TLR9 cDNA. SEQ ID NO:32 is a nucleotide sequence of murine cDNA encoding amino acids 1-821 of SEQ ID NO:29.

An amino acid sequence of human TLR9 is available as GenBank accession no. AAF78037, provided as SEQ ID NO:33. Amino acids numbered 1-820 of SEQ ID NO:33 presumptively include the entire extracellular domain and correspond to SEQ ID NO:34. SEQ ID NO:35 corresponds to GenBank accession number AF245704, which is a nucleotide sequence of human TLR9 cDNA. SEQ ID NO:36 is a nucleotide sequence of human cDNA encoding amino acids 1-820 of SEQ ID NO:33.

#### SEQ ID NO:29 (Murine TLR9)

MVLRRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI  
 15 HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCHMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSL  
 SHTNIVLDANSLAGLYSLRVLFMDGNCYKPNCTGAVKVTPGALLGLSNLTHLSLKYNNTKVPRQLPPSLEYL  
 LVSYNLIVKLGPEDLANLTSLRVLDVGGNCRCDHAPNPCIECGQKSLHLHPETFHHLSHLEGLVLKDSSLHTLN  
 SSWFQGLVNLSVLDLSENFLYESINHTNAFQNLTRLRKLNLNLSFNRYKKVSFARLHLASSFKNLVSLQELNMNGIF  
 20 FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSDNRISGPSTLSEATPEEADDAEQEELL  
 SADPHAPLSTPASKNFMDCRKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ  
 VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFMSKGIGHNFSFVAHLSMLHSLSLAHNDIHRVSSHLNSNS  
 VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNNLHILRPQNLDNLPKSLKLLSLRDNYLSFFNWTSL  
 FLNLEVLDDLQALNQLKALTNGTLPNGTLLQKLDVSSNSIVSVVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV  
 25 MNLTVLDVRSNPLHCACGAADFVLLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFGLSLL  
 AVAVGMVVPILHHLCGWDVWYCFHLCLAWPLLLARSRRSAQALPYDAFVVDKAQSAVADWVYNELRVRLERRG  
 RRALRLCLEDRDWLPQTLFENLWASIYGSRTFLVLAHTDRVSGLLRTSFLLAQQRLLDRKDVVVLVILRPDA  
 HRSRYVRLRQLRCRQSVLFWPQQPNGQGFWAQLSTALTRDNRHFYNQNFRCRGPTAE

#### SEQ ID NO:30 (Murine TLR9)

MVLRRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI  
 30 HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCHMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSL  
 SHTNIVLDANSLAGLYSLRVLFMDGNCYKPNCTGAVKVTPGALLGLSNLTHLSLKYNNTKVPRQLPPSLEYL  
 LVSYNLIVKLGPEDLANLTSLRVLDVGGNCRCDHAPNPCIECGQKSLHLHPETFHHLSHLEGLVLKDSSLHTLN  
 SSWFQGLVNLSVLDLSENFLYESINHTNAFQNLTRLRKLNLNLSFNRYKKVSFARLHLASSFKNLVSLQELNMNGIF  
 35 FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSDNRISGPSTLSEATPEEADDAEQEELL  
 SADPHAPLSTPASKNFMDCRKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ  
 VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFMSKGIGHNFSFVAHLSMLHSLSLAHNDIHRVSSHLNSNS  
 VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNNLHILRPQNLDNLPKSLKLLSLRDNYLSFFNWTSL  
 FLNLEVLDDLQALNQLKALTNGTLPNGTLLQKLDVSSNSIVSVVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV  
 40 MNLTVLDVRSNPLHCACGAADFVLLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFG

#### SEQ ID NO:31 (Murine TLR9)

tgtcagagggagcctcgggagaatcctccatctcccaacatggttctccgtcgaaggactctgcaccccttgctcc  
 ctctctggtacaggctgcagtgctggtgagactctggccctgggtaccctgcctgccttctaccctgtgagctg

- 25 -

aagcctcatggcctgggtggactgcaattggctgttctctgaagtctgtaccccggttctctgcggcagcatcctgc  
tccaacatcaccgcctctccttgatctccaaccgtatccaccacctgcacaactccgacttcgtccacctgtcc  
aacctgcggcagctgaacctcaagtggaaactgtccaccacactggccttagccccctgcacttctcttgccacatg  
accattgagcccgagaaccttctctggctatgcgtacactggaggagctgaacctgagctataatgggtatcaccact  
5 gtgccccgactgcccagctcctctgggtgaatctgagcctgagccacaccaatcctgggttctagatgctaacagc  
ctcgccggcctatacagcctgcgcgttctcttcatggacgggaactgtactacaagaacctcctgcacaggagcg  
gtgaaggtagccccagcgccctcctgggcctgagcaatctcaccatctgtctctgaagtataacaacctcaca  
aagggtccccgccaactgccccccagcctggagtaacctcctgggtgtcctataacctcattgtcaagctggggcct  
gaagacctggccaatctgacctcctctcgagtaacttgatgtgggtgggaattgcccgtcgctgcgacctgcccc  
10 aatcctctgtagaatgtggccaaaagtccctccacctgcacctgagaccttccatcacctgagccatctggaa  
ggcctgggtgctgaaggacagctctctccatacactgaactcttctgggttccaaggctgtggtcaacctctcggtg  
ctggacctaaagcgagaacttctctatgaaagcatcaaccacaccaatgccttccagaacctaacccgcctgcgc  
aagctcaacctgtccttcaattaccgcaagaaggtatcctttgcccgcctccacctggcaagttccttcaagaac  
ctgggtgtcactgcaggagctgaacatgaacggcatcttcttccgctcgctcaacaagtaacagctcagatggctg  
15 gccgatctgccccaaactccacactctgcactcttcaaatgaacttcatcaaccaggcacagctcagcatctttgggt  
accttccgagcccttccgcttcttgggacttgcagacaatcgcatcagtgggccttcaacgctgtcagaagccacc  
cctgaagaggcagatgatgcagagcaggaggagctgtgtctgcggatcctcaccagctccactgagcaccct  
gcttctaagaacttcatggacaggtgtaagaacttcaagttcaccatggacctgtctcggaacaacctgggtgact  
atcaagccagagatgtttgtcaatctctcagcctccagtgcttagcctgagccacaactccattgcacaggct  
20 gtcaatggctctcagttcctgcccgtgactaatctgcaggtgctggacctgtccataacaacctggacttgtac  
cactggaaatcggtcagtgagctaccacagttgcaggccctggacctgagctacaacagccagccctttagcatg  
aagggtataggccacaatttcagtttctgtggccatctgtccatgtcacacagccttagcctggcacacaatgac  
attcataccgctgtgtcctcactctcaacagcaactcagtgaggttcttgaacttcagcggcaacgggtatgggc  
cgcatgtgggatgaggggggcttcttctccatttcttccaaggcctgagtgggcctgctgaagctggacctgtct  
25 caaaataacctgcatactcctccggccccagaaaccttgacaacctccccagagcctgaagctgctgagcctccga  
gacaactacctatcttcttactggaccagtctgtccttcttgcaccaacctggaagtcctagacctggcaggc  
aaccagctaaaggccctgaccaatggcaccctgcctaattggcaccctcctccagaaactggatgtcagcagcaac  
agtatcgtctctgtgggtcccagccttcttccgctctggcggtcgagctgaaagaggtcaacctcagccacaacatt  
ctcaagacgggtggatcgctcctgggttggggccattgtgatgaacctgacagttctagacgtgagaagcaacct  
30 ctgcatctgtcctgtggggcagccttcgttagacttactgttggaggtgcagaccaaggtgcctggcctggcta  
gggtgtgaagtgtggcagccccggccagctgcaggccgtagcatcttgcacaggacctgcgctgtgcctggat  
gaggtcctctcttgggactgcttggccttctactcttggctgtggcctggtggcctggtgctatactgcac  
catctctgcggtgggactgctggtactgttttcatctgtgctggcatggctaccttctgtggcccgagccga  
cgcagcgcccaagctctcccctatgatgccttctgtgttctgataaggcacagagcgcagttgcccactgggtg  
35 tataacgagctgcgggtgcggtggaggagcggcggtgcggcagccctacgcttgtgtctggaggaccgagat  
tggctgctggccagacgctcttcgagaacctctgggcttccatctatgggagccgcaagactctatttgtgctg  
gcccacacggaccgcgtcagtgccctcctgcgcaccagcttcttctgtggtcagcagcgctgttgaagaccgc  
aaggacgtggtggttgggtgatcctgcgtccggatgccaccgctcccgtatgtgagctgcgccagcgtctc  
tgccgcagagtggtgctcttctggccagcagcccaacggggcagggggcttctggggccagctgagtaagacc  
40 ctgactagggaacaaccgcaacttctataaccagaacttctgcccgggacctacagcagaatagctcagagcaaca  
gctggaaacagctgcactcttcatgctgggttcccagagttgctctgctgc

## SEQ ID NO:31 (Murine TLR9)

atgggttctccgtcgaaggactctgcaccccttgtccctcctggtagaggtgcagtgtggctgagactctggcc  
45 ctgggtaccctgcctgccttctaccctgtgagctgaagcctcatggcctgggtggactgcaattggctgttcttg  
aagtctgtaccccggttctctgcggcagcatcctgctccaacatcaccgcctctccttgatctccaaccgtatc  
caccacctgcacaactccgacttcgtccacctgtccaacctgcccagctgaacctcaagtggaaactgtccacc  
actggccttagccccctgcacttctcttgccacatgaccttagcccagaaccttcttggtatgctgactg  
gaggagctgaacctgagctataatgggtatcaccactgtgccccgactgcccagctccctgggtgaatctgagcctg  
50 agccacaaccaacatcctgggtctagatgtcaacagcctgcggcgctatacagcctgcgcgttctcttcatggac  
gggaactgtactacaagaacctcgcacaggagcgggtgaaggtgacccaggcgccctcctgggcctgagcaat  
ctcaccatctgtctctgaagtataacaacctcacaagggtgccccgccaactgccccagcctggagtacctc  
ctgggtgctctataacctcattgtcaagctggggcctgaagacctggccaatctgacctccttctgagtacttgat  
gtgggtgggaattgcccgtcgctgcgacctgcccccaatccctgtatagaatgtggccaaaagtccctccacctg  
55 caccctgagaccttccatcacctgagccatctggaaggcctgggtgctgaaggacagctctctccatacactgaac  
tcttctgggttccaaggctgggtcaacctctcggtgctggacctaaagcgagaacttctctatgaaagcatcaac  
cacaccaatgccttccagaacctaacccgcctgcgcaagctcaacctgtccttcaattaccgcaagaaggtatcc



- 26 -

tttgcccgcctccacctggcaagttccttcaagaacctgggtgtcactgcaggagctgaacatgaacggcatcttc  
 ttcgctcgtcaacaagtacacgctcagatggctggccgatctgcccactccacactctgcatcttcaaatg  
 aacttcatcaaccaggcacagctcagcatctttggtaccttcgagcccttcgctttgtggacttgtcagacaat  
 5 cgcacagtgggccttcaacgctgtcagaagccacctgaagaggcagatgatgcagagcaggaggagctgttg  
 tctgcgatcctcaccagctccactgagcaccctgcttctaagaacttcatggacaggtgtagaacttcaag  
 ttcccatggagctgtctcggaacaacctgggtgactatcaagccagagatgtttgtcaatctctcacgcctccag  
 tgtcttagcctgagccacaaactccattgcacaggctgtcaatggctctcagttcctgcccgtgactaactctgcag  
 gtgctggacctgtccataaaaaactggacttgtaccactggaaatcggtcagtgagctaccacagttgcaggcc  
 ctggacctgagctacaacagccagcccttagcatgaagggtataggccacaatttcagttttgtggcccatctg  
 10 tccatgctacacagccttagcctggcacacaatgacattcataccctgtgtcctcacatctcaacagcaactca  
 gtgaggtttcttgacttcagcggcaacgggtatgggcccagatgtgggatgagggggccctttatctccatttcttc  
 caaggcctgagtggcctgctgaagctggacctgtctcaaaataacctgcatactcctcgggccccaagaacctgac  
 aacctcccaagagcctgaagctgctgagcctccgagacaactacctatcttctttaactggaccagtctgtcc  
 ttcttgcaccaactggaagtcttagacctggcaggcaaccagctaaaggccctgaccaatggcaccctgcctaact  
 15 ggcaccctcctccagaactggatgtcagcagcaacagatctcgtctctgtggtcccagccttcttgcctctggcg  
 gtcgagctgaaagaggtcaacctcagccacaacattctcaagacggtggatcgctcctggtttgggcccattgtg  
 atgaacctgacagttctagacgtgagaagcaacctctgcactgtgctgtggggcagccttcgtagacttactg  
 ttggaggtgcagaccaaggtgctggcctggctaaggtgtgaagtgtggcagccccggccagctgcaggggcgt  
 agcatcttcgcacaggacctgcggctgtgcctggatgaggtcctctcttgggactgctttggc  
 20

## SEQ ID NO:33 (Human TLR9)

MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRI  
 HHLHDSDFAHLPRLRLNLKWNCPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL  
 25 SHTNIMLSDASLAGLHALRFLFMDGNCYKPNCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYL  
 LLSYNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNCPMECPRHFPQLHPDTFSLSLRLEGLVLKDSSLSWLN  
 ASWFRGLGNLRVLDLSENFLYKCIITKTKAFQGLTQLRKLNLFSFNYQKRVSAHLSLAPSFGLVALKELDMHGIF  
 FRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSNRI SGASELTATMGEADGGEKVLQ  
 GD LAPAPVDT PSED FRPNCSTLNFTLDLSRNNLVTVP EMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV  
 30 LDLSRNKLDLYHEHSFTELPRLEALDLSYNSQPFQMGGVGHNF SFVAHLRTRLRHL SLAHNNIHSQVSQQLCSTSL  
 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNLRLHTLLPQTLRNLPKSLQVLRRLDNYLAFFKWWSLHF  
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRLRLDVCNSISFVAPGFFSKAKELRELNL SANALKTVDSWFGPLAS  
 ALQILDVSANPLHCACGAAMDFLLEVQAAVPGLP SRVKCGSPGQLQGLSIFAQDLRLCLDEALS WDCFA  
 VALGLGVPMHLHLCGWDLYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVDKTS AVADWVYNELRGQLEECRG  
 35 RWALRLCLEERDWPGLKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLDRKDVVVLVILSPDG  
 RRSRYVRLRQLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHFFYNRNF CQGPTAE

## SEQ ID NO:34 (Human TLR9)

MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRI  
 HHLHDSDFAHLPRLRLNLKWNCPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL  
 40 SHTNIMLSDASLAGLHALRFLFMDGNCYKPNCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYL  
 LLSYNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNCPMECPRHFPQLHPDTFSLSLRLEGLVLKDSSLSWLN  
 ASWFRGLGNLRVLDLSENFLYKCIITKTKAFQGLTQLRKLNLFSFNYQKRVSAHLSLAPSFGLVALKELDMHGIF  
 FRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSNRI SGASELTATMGEADGGEKVLQ  
 45 GD LAPAPVDT PSED FRPNCSTLNFTLDLSRNNLVTVP EMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV  
 LDLSRNKLDLYHEHSFTELPRLEALDLSYNSQPFQMGGVGHNF SFVAHLRTRLRHL SLAHNNIHSQVSQQLCSTSL  
 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNLRLHTLLPQTLRNLPKSLQVLRRLDNYLAFFKWWSLHF  
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRLRLDVCNSISFVAPGFFSKAKELRELNL SANALKTVDSWFGPLAS  
 ALQILDVSANPLHCACGAAMDFLLEVQAAVPGLP SRVKCGSPGQLQGLSIFAQDLRLCLDEALS WDCFA

## 50 SEQ ID NO:35 (Human TLR9)

aggctggtataaaaatcttacttctctattctctgagccgctgctgcccctgtgggaaggacctcgagtgtga  
 agcatcttccctgtagctgctgtccagctgtcccgcagaccctctggagaagccctgccccccagcatgggt  
 ttctgcccgcagcgcctgcacccgctgtctctcctgggtgcaggccatcatgctggccatgacctggccctgggt



accttgccctgecttccctaccctgtgagctccagccccacggcctggtgaactgcaactggctgttccctgaagtct  
 gtgccccacttctccatggcagcacccccgtggcaatgtcaccagcctttccttgtcctccaaccgcatccaccac  
 ctccatgattctgactttgcccacctgcccagcctgcccgcctctcaacctcaagtggaaactgcccgcgggttggc  
 ctgagccccatgcacttcccctgccacatgacctcgagcccagcaccttcttggctgtgcccaccctggaagag  
 5 ctaaacctgagctacaacaacatcatgactgtgctgcgctgccc aaatccctcatatccctgtccctcagccat  
 accaaccatcctgatgtagactctgcccagcctcgccggcctgcatgcccctgcgcttccctattcatggacggcaac  
 tgttattacaagaacccctgcaggcaggcactggaggtggccccgggtgcccctccttggcctgggcaacctcacc  
 cacctgtcactcaagtacaacaacctcactgtgggtgccccgcaacctgcccctccagcctggagtatctgtgttg  
 tcctacaaccgcatcgtaaaactggcgctgaggacctggccaatctgaccgcccctgctgtgtgctcgatgtgggc  
 10 ggaaattgcccgcgctgcgaccacgctcccaacccctgcatggagtgcctcgtcacttccccagctacatccc  
 gataccttcagccacctgagccgtcttgaaggcctgggtgttgaaggacagtctctctcctggctgaatgccagt  
 tgggtccgtgggtgggaaacctccgagtgctggacctgagtgagaacttccctctacaaatgcatcactaaaacc  
 aaggccttccagggcctaacacagctgcgcaagcttaacctgtccttcaattaccaaagagggtgtcctttgcc  
 cacctgtctctggccccttcccttggggagcctgggtcgccctgaaggagctggacatgcacggcatcttcttccgc  
 15 tcaactcgatgagaccagctccggccactggcccgcctgcccagctcctcagactctgctgtgcagatgaacttc  
 atcaaccaggcccagctcgccatcttccagggccttcccctggcctgctacgtggacctgtcggacaaccgcatc  
 agcggagcttccggagctgacagccacctgggggagggagctggaggggagaaggctggctgagcctggggac  
 ctgtctccggcccagtgaggacactcccagctctgaagacttcaggcccaactgcagcacctcaacttcaccttg  
 gatctgtcacggaacaacctggtagccgtgcagccggagatgtttgcccagctctcgcacctgcagtgccctgcgc  
 20 ctgagccacaactgcatctcgcaggcagtc aatggctcccagttcctgcccgtgaccggtctgcaggtgctagac  
 ctgtcccgaataagctggacctctaccacgagcactcattcacggagctaccgcgactggaggccctggacctc  
 agctacaacagccagccccttggcatgcagggcggtgggccacaacttcagcttctgtggctcacctgcccacccctg  
 cgccacctcagcctggcccacaacaacatccacagccaagtgtcccagcagctctgcagtaagctgcgtgcccggcc  
 ctggacttcagcggcaatgcactgggccatagtggggccgagggagacctctatctgacttcttccaaggcctg  
 25 agcggtttgatctggctggacttgtcccagaaccgctgacacccctcctgccc aaacccctgcgcaacctcccc  
 aagagcctacaggtgctgcttccgtgacaattacctggccttctttaagtgggtggagcctccacttccctgcc  
 aaactggaagtccctgcacctggcaggaaaccggctgaaggccctgaccaatggcagcctgctgctggcaccgg  
 ctccggaggctggatgtcagctgcaacagcatcagcttccgtggccccggcttcttttccaaggccaaggagctg  
 cgagagctcaaccttagcgcgaacgcccctcaagacagtgaggacctcctgggttggggcccctggcgagtgccctg  
 30 caaatactagatgtaagcgccaacctctgcactgcgcctgtggggcgcccttatggacttccctgctggaggtg  
 caggctgcccgtgcccggctgcccagccgggtgaagtgtggcagtcggggccagctccaggccctcagcatctt  
 gcacaggacctgcgcctctgctggatgaggccctcctgggactgttccgcccctcctgctggctgtgggt  
 ctgggcttgggtgtgcccctgctgcatcacctctgtggctgggacctctgggtactgcttccacctgtgcccggcc  
 tggcttccctggcgggggcggaagtggggcgagatgaggatgcccctgcccctacgatgccttctgtggtcttcgac  
 35 aaaacgcagagcgcagtgaggcagactgggtgtacaacgagcttccggggcagctggaggagtgcctggggcgctgg  
 gcactccgctgtgcttggaggaaacgcgactggctgcctggcaaaacctcttggagaacctgtggggcctcggtc  
 tatggcagccgcaagacgctgttgtgtggtggcccacacggacccgggtcagtggtctcttgcgcgccagcttccctg  
 ctggcccagcagcgcctgctggaggaccgcaaggacgtcgtgggtgctgggtgatcctgagccctgacggccgcccgc  
 tcccgtacgtgcccgtgcgccagcgcctctgcgcagagatgtcctcctctggcccaccagccaggtggtcag  
 40 cgcagcttctggggccagctgggcatggccctgaccagggaacaccacacttctataaccgcaactctgtgccag  
 ggaccacaggccgaatagccgtgagccggaatcctgcaggtgccacctccacactcacctcacctctgctgccc  
 tggctgacctccccctgctgcctccctcaccacacacctgacacagagca

## SEQ ID NO:36 (Human TLR9)

atgggtttctgcccagcgccttgcaaccgctgtctctcctgggtgcaggccatcatgctggccatgacctggcc  
 ctgggtaccttgccctgecttccctaccctgtgagctccagccccacggcctggtgaactgcaactggctgttccctg  
 aagtctgtgccccacttctccatggcagcacccccgtggcaatgtcaccagcctttccttgtcctccaaccgcatc  
 caccacctccatgattctgactttgcccacctgcccagcctgcccgcctctcaacctcaagtggaaactgcccgcg  
 gttggcctcagccccatgcacttcccctgccacatgacctcgagcccagcaccttcttggctgtgcccaccctg  
 50 gaagagctaaacctgagctacaacaacatcatgactgtgctgcgctgccc aaatccctcatatccctgtccctc  
 agccataaccaatcctgatgctagactctgcagcctcgccggcctgcatgcccctgccccttccctattcatggac  
 ggcaactgttattacaagaacccctgcaggcaggcactggaggtggccccgggtgcccctccttggcctgggcaac  
 ctccccacctgtcactcaagtacaacaacctcactgtgggtgccccgcaacctgcccctccagcctggagtatctg  
 ctgttctctacaaccgcatcgtaaaactggcgccctgaggacctggccaatctgaccgcccctgctgtgtcgtgat  
 55 gtggggcgaaaattgcccgcgctgcgaccacgctcccaacccctgcatggagtgcctcgtcacttccccagcta  
 catcccgataccttcagccacctgagccgtcttgaaggcctgggtgttgaaggacagtctctctcctggctgaat  
 gccagttgggtccgtgggtgggaaacctccgagtgctggacctgagtgagaacttccctctacaaatgcatcact

- 28 -

aaaaccaaggccttccagggcctaacacagctgcgcaagcttaacctgtccttcaattacaaaaagaggggtgtcc  
 tttgcccacctgtctctggcccttccttcgggagcctggctgcctgaaggagctggacatgcacggcatcttc  
 ttccgctcactcgatgagaccagctccggccactggccgctgccatgctccagactctgcgtctgcagatg  
 aacttcatcaaccaggcccagctcggcatcttcagggccttcctggcctgcgtacgtggacctgtcggacaac  
 5 cgcatcagcggagcttcggagctgacagccaccatgggggaggcagatggaggggagaaggtctggctgcagcct  
 ggggacctgtcctcgccccagtggaactcccagctctgaagacttcaggcccaactgcagcaccctcaacttc  
 accttggatctgtcaggaacaacctggtgaccgtgcagccggagatgtttgcccagctctcgcacctgcagtgc  
 ctgcgccctgagccacaactgcatctcgcaggcagtcgaatggctcccagttcctgcccgtgaccggtctgcaggtg  
 ctagacctgtcccgaataagctggacctctaccacgagcactcattcacggagctaccgcgactggagggcctg  
 10 gacctcagctacaacagccagccctttggcatgcaggcgctggggccacaacttcagcttctggtgctcacctgcgc  
 accctgcgccacctcagcctggcccaacaacatccacagccaagtgtcccagcagctctgcagtacgtcgtg  
 cggggcctggacttcagcggcaatgcactggggccatatgtggggcgaggagacctctatctgcacttcttccaa  
 ggccctgagcggtttgatctggctggactgtcccagaaccgcctgcacaccctcctgccccaaacctgcgcaac  
 ctccccaaagagcctacaggtgctgcgtctccgtgacaattacctggccttctttaagtggtggagcctccacttc  
 15 ctgccccaaactggaagtctcgcacctggcaggaaccggctgaaggccctgaccaatggcagcctgcctgctggc  
 acccggtccggaggtggatgtcagctgcaacagcatcagcttcgtggccccggcttcttttccaaggccaag  
 gagctgcgagagctcaaccttagcgccaacgcctcaagacagtgaggaccactcctggtttggccctggcgagt  
 gccctgcaataactagatgtaagcgccaacctctgcactgcgcctgtggggcgccctttatggacttctgctg  
 gaggtgcaggtgcgctgcccggctgtcccagccgggtgaagtgtggcagtcggggccagctccagggcctcagc  
 20 atctttgcacaggacctgcgcctctgcctggatgaggccctctcctgggactgtttcgcc

In addition to the foregoing native rat, porcine, bovine, equine, and ovine TLR9  
 polypeptides and nucleic acid molecules encoding them, chimeric TLR9 polypeptides and  
 nucleic acid molecules encoding them are provided by the invention. The chimeric  
 25 polypeptides include at least one amino acid substitution based on a comparison of  
 conserved and non-conserved amino acids among at least two of rat, murine, porcine, bovine,  
 equine, ovine, canine, feline, and human TLR9. The information contained in a multiple  
 sequence alignment of these various TLR9 polypeptide sequences, provided for example in  
 Figure 1, can be used to identify and select individual amino acid positions and even  
 30 individual amino acids to substitute in designing a chimeric TLR9. The substitution or  
 substitutions can be effected using methods known to those of ordinary skill in molecular  
 biology. Nucleic acids encoding the native or chimeric polypeptides of the invention can be  
 inserted into an expression vector and used to express TLR9 polypeptide.

A conservative amino acid substitution shall refer to a substitution of a first amino  
 35 acid for a second amino acid, wherein side chains of the first amino acid and the second  
 amino acid share similar features in terms of hydrophobicity, size, aromaticity, or tendency to  
 alter conformation. For example, conservative amino acid substitutions generally may be  
 made between members within each of the following groups: hydrophobic (A, I, L, M, V),  
 neutral (C, S, T), acidic (D, E), basic (H, K, N, Q, R), and aromatic (F, W, Y). A non-  
 40 conservative amino acid substitution refers to any other amino acid substitution.

- 29 -

An expression vector for TLR9 will include at least a nucleotide sequence coding for a TLR9, or a fragment thereof coding for a functional TLR9 polypeptide, operably linked to a gene expression sequence which can direct the expression of the TLR9 nucleic acid within a eukaryotic or prokaryotic cell. A "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the nucleic acid to which it is operably linked. With respect to TLR9 nucleic acid, the "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the TLR9 nucleic acid to which it is operably linked. The gene expression sequence may, for example, be a mammalian or viral promoter, such as a constitutive or inducible promoter. Constitutive mammalian promoters include, but are not limited to, the promoters for the following genes: hypoxanthine phosphoribosyl transferase (HPRT), adenosine deaminase, pyruvate kinase,  $\beta$ -actin promoter, and other constitutive promoters. Exemplary viral promoters which function constitutively in eukaryotic cells include, for example, promoters from the simian virus (e.g., SV40), papillomavirus, adenovirus, human immunodeficiency virus (HIV), Rous sarcoma virus (RSV), cytomegalovirus (CMV), the long terminal repeats (LTR) of Moloney murine leukemia virus and other retroviruses, and the thymidine kinase (TK) promoter of herpes simplex virus. Other constitutive promoters are known to those of ordinary skill in the art. The promoters useful as gene expression sequences of the invention also include inducible promoters. Inducible promoters are expressed in the presence of an inducing agent. For example, the metallothionein (MT) promoter is induced to promote transcription and translation in the presence of certain metal ions. Other inducible promoters are known to those of ordinary skill in the art.

In general, the gene expression sequence shall include, as necessary, 5' non-transcribing and 5' non-translating sequences involved with the initiation of transcription and translation, respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribing sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined nucleic acid coding sequence for a TLR9 polypeptide. The gene expression sequences optionally include enhancer sequences or upstream activator sequences as desired.

- 30 -

Generally a nucleic acid coding sequence and a gene expression sequence are said to be “operably linked” when they are covalently linked in such a way as to place the transcription and/or translation of the nucleic acid coding sequence under the influence or control of the gene expression sequence. Thus the TLR9 nucleic acid coding sequence and the gene expression sequence are said to be “operably linked” when they are covalently linked in such a way as to place the transcription and/or translation of the TLR9 nucleic acid coding sequence under the influence or control of the gene expression sequence. If it is desired that the TLR9 sequence be translated into a functional protein, two DNA sequences are said to be operably linked if induction of a promoter in the 5' gene expression sequence results in the transcription of the TLR9 sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the TLR9 sequence, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a gene expression sequence would be operably linked to a TLR9 nucleic acid sequence if the gene expression sequence were capable of effecting transcription of that TLR9 nucleic acid sequence such that the resulting transcript might be translated into the desired TLR9 protein or polypeptide.

A “TLR9 ligand” as used herein refers to a molecule that specifically binds a TLR9 polypeptide. In one embodiment the TLR9 ligand specifically binds a TLR9 polypeptide corresponding to at least a ligand-binding portion of the extracellular domain of TLR9. In most instances a TLR9 ligand will also induce TLR9 signaling when contacted with TLR9 under suitable conditions. TLR9 signaling refers to TLR/IL-1R signal transduction mediated through the TLR9, as described in further detail elsewhere herein. As mentioned above, CpG nucleic acids have been reported to be TLR9 ligands, but TLR9 ligands may include other entities as well, including, for example, small molecules. As also previously mentioned, there appears to be a species-specific preference for at least certain TLR9s and certain CpG motifs. As used herein, a species-preferred CpG DNA refers to a particular CpG DNA that is optimized for signal induction by a TLR9 of a particular species. A CpG DNA that is optimized for signal induction by a TLR9 of a particular species refers to a CpG DNA having a sequence that preferentially binds to and/or induces signaling by TLR9 of that species. For example, a human-preferred CpG DNA shall refer to a CpG DNA that optimally stimulates human TLR9 to signal through its TIR domain. Likewise, a murine-preferred CpG DNA

- 31 -

shall refer to a CpG DNA that optimally stimulates murine TLR9 to signal through its TIR domain. Examples of human-preferred and murine-preferred CpG DNA are ODN 2006 (SEQ ID NO:58) and 1668 (SEQ ID NO:60), respectively.

5 The binding and species specificity of TLR9s are believed to be influenced by key amino acids present in the extracellular domain of TLR9. Key amino acids in a TLR9 as used herein refer to those amino acids which contribute significantly to ligand binding and ligand specificity of a particular TLR9 polypeptide.

A "CpG nucleic acid" or a "CpG immunostimulatory nucleic acid" as used herein is a nucleic acid containing at least one unmethylated CpG dinucleotide (cytosine-guanine  
10 dinucleotide sequence, i.e., "CpG DNA" or DNA containing a 5' cytosine followed by 3' guanine and linked by a phosphate bond) which activates a component of the immune system. The entire CpG nucleic acid can be unmethylated or portions may be unmethylated but at least the C of the 5' CG 3' must be unmethylated.

In one embodiment a CpG nucleic acid is represented by at least the formula:

15 
$$5'-N_1X_1CGX_2N_2-3'$$

wherein  $X_1$  and  $X_2$  are nucleotides, N is any nucleotide, and  $N_1$  and  $N_2$  are nucleic acid sequences composed of from about 0-25 N's each. In some embodiments  $X_1$  is adenine, guanine, or thymine and/or  $X_2$  is cytosine, adenine, or thymine. In other embodiments  $X_1$  is cytosine and/or  $X_2$  is guanine.

20 Nucleic acids having modified backbones, such as phosphorothioate backbones, also fall within the class of immunostimulatory nucleic acids. U.S. Pat. Nos. 5,723,335 and 5,663,153 issued to Hutcherson, et al. and related PCT publication WO95/26204 describe immune stimulation using phosphorothioate oligonucleotide analogues. These patents describe the ability of the phosphorothioate backbone to stimulate an immune response in a  
25 non-sequence specific manner.

An immunostimulatory nucleic acid molecule, including for example a CpG DNA, may be double-stranded or single-stranded. Generally, double-stranded molecules may be more stable *in vivo*, while single-stranded molecules may have increased activity. The terms "nucleic acid" and "oligonucleotide" refer to multiple nucleotides (i.e., molecules comprising  
30 a sugar (e.g., ribose or deoxyribose) linked to a phosphate group and to an exchangeable organic base, which is either a substituted pyrimidine (e.g., cytosine (C), thymine (T) or uracil (U)) or a substituted purine (e.g., adenine (A) or guanine (G)) or a modified base. As

- 32 -

used herein, the terms "nucleic acid" and "oligonucleotide" refer to oligoribonucleotides as well as oligodeoxyribonucleotides. The terms shall also include polynucleosides (i.e., a polynucleotide minus the phosphate) and any other organic base-containing polymer. The terms "nucleic acid" and "oligonucleotide" also encompass nucleic acids or oligonucleotides with a covalently modified base and/or sugar. For example, they include nucleic acids having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 2' position and other than a phosphate group at the 5' position. Thus modified nucleic acids may include a 2'-O-alkylated ribose group. In addition, modified nucleic acids may include sugars such as arabinose instead of ribose. Thus the nucleic acids may be heterogeneous in backbone composition thereby containing any possible combination of polymer units linked together such as peptide-nucleic acids (which have amino acid backbone with nucleic acid bases). In some embodiments the nucleic acids are homogeneous in backbone composition.

The substituted purines and pyrimidines of the immunostimulatory nucleic acids include standard purines and pyrimidines such as cytosine as well as base analogs such as C-5 propyne substituted bases. Wagner RW et al. (1996) *Nat Biotechnol* 14:840-4. Purines and pyrimidines include but are not limited to adenine, cytosine, guanine, thymine, 5-methylcytosine, 2-aminopurine, 2-amino-6-chloropurine, 2,6-diaminopurine, hypoxanthine, and other naturally and non-naturally occurring nucleobases, substituted and unsubstituted aromatic moieties.

The immunostimulatory nucleic acid is a linked polymer of bases or nucleotides. As used herein with respect to linked units of a nucleic acid, "linked" or "linkage" means two entities are bound to one another by any physicochemical means. Any linkage known to those of ordinary skill in the art, covalent or non-covalent, is embraced. Such linkages are well known to those of ordinary skill in the art. Natural linkages, which are those ordinarily found in nature connecting the individual units of a nucleic acid, are most common. The individual units of a nucleic acid may be linked, however, by synthetic or modified linkages.

Whenever a nucleic acid is represented by a sequence of letters it will be understood that the nucleotides are in 5' to 3' (or equivalent) order from left to right and that "A" denotes adenine, "C" denotes cytosine, "G" denotes guanine, "T" denotes thymidine, and "U" denotes uracil unless otherwise noted.

- 33 -

Immunostimulatory nucleic acid molecules useful according to the invention can be obtained from natural nucleic acid sources (e.g., genomic nuclear or mitochondrial DNA or cDNA), or are synthetic (e.g., produced by oligonucleotide synthesis). Nucleic acids isolated from existing nucleic acid sources are referred to herein as native, natural, or isolated nucleic acids. The nucleic acids useful according to the invention may be isolated from any source, including eukaryotic sources, prokaryotic sources, nuclear DNA, mitochondrial DNA, etc. Thus, the term nucleic acid encompasses both synthetic and isolated nucleic acids.

The immunostimulatory nucleic acids can be produced on a large scale in plasmids, (see *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989) and separated into smaller pieces or administered whole. After being administered to a subject the plasmid can be degraded into oligonucleotides. One skilled in the art can purify viral, bacterial, eukaryotic, etc. nucleic acids using standard techniques, such as those employing restriction enzymes, exonucleases or endonucleases.

For use in the instant invention, the immunostimulatory nucleic acids can be synthesized *de novo* using any of a number of procedures well known in the art. For example, the  $\beta$ -cyanoethyl phosphoramidite method (Beaucage SL and Caruthers MH, *Tetrahedron Let* 22:1859 (1981)); nucleoside H-phosphonate method (Garegg et al., *Tetrahedron Let* 27:4051-4054 (1986); Froehler et al., *Nucl Acid Res* 14:5399-5407 (1986); Garegg et al., *Tetrahedron Let* 27:4055-4058 (1986); Gaffney et al., *Tetrahedron Let* 29:2619-2622 (1988)). These chemistries can be performed by a variety of automated oligonucleotide synthesizers available in the market.

The immunostimulatory nucleic acid may be any size of at least 6 nucleotides but in some embodiments are in the range of between 6 and 100 or in some embodiments between 8 and 35 nucleotides in size. Immunostimulatory nucleic acids can be produced on a large scale in plasmids. These may be administered in plasmid form or alternatively they can be degraded into oligonucleotides before administration.

A "stabilized immunostimulatory nucleic acid" shall mean a nucleic acid molecule that is relatively resistant to *in vivo* degradation (e.g., via an exo- or endo-nuclease).

Stabilization can be a function of length or secondary structure. Nucleic acids that are tens to hundreds of kbs long are relatively resistant to *in vivo* degradation. For shorter nucleic acids, secondary structure can stabilize and increase their effect. For example, if the 3' end of an

- 34 -

oligonucleotide has self-complementarity to an upstream region, so that it can fold back and form a sort of stem loop structure, then the oligonucleotide becomes stabilized and therefore exhibits more activity.

Some stabilized immunostimulatory nucleic acids have a modified backbone. It has  
5 been demonstrated that modification of the oligonucleotide backbone provides enhanced activity of the immunostimulatory nucleic acids when administered *in vivo*. Nucleic acids, including at least two phosphorothioate linkages at the 5' end of the oligonucleotide and multiple phosphorothioate linkages at the 3' end, preferably 5, may provide maximal activity and protect the oligonucleotide from degradation by intracellular exo- and endo-nucleases.  
10 Other modified oligonucleotides include phosphodiester modified oligonucleotide, combinations of phosphodiester and phosphorothioate oligonucleotide, methylphosphonate, methylphosphorothioate, phosphorodithioate, and combinations thereof. Each of these combinations and their particular effects on immune cells is discussed in more detail in U.S. Pat. Nos. 6,194,388 and 6,207,646, the entire contents of which are incorporated herein by  
15 reference. It is believed that these modified oligonucleotides may show more stimulatory activity due to enhanced nuclease resistance, increased cellular uptake, increased protein binding, and/or altered intracellular localization. Both phosphorothioate and phosphodiester nucleic acids are active in immune cells.

Other stabilized immunostimulatory nucleic acids include: nonionic DNA analogs,  
20 such as alkyl- and aryl-phosphates (in which the charged phosphonate oxygen is replaced by an alkyl or aryl group), phosphodiester and alkylphosphotriesters, in which the charged oxygen moiety is alkylated. Oligonucleotides which contain diol, such as tetraethyleneglycol or hexaethyleneglycol, at either or both termini have also been shown to be substantially resistant to nuclease degradation.

25 Phosphorothioate nucleic acid molecules may be synthesized using automated techniques employing either phosphoramidate or H-phosphonate chemistries. Aryl- and alkyl-phosphonates can be made, e.g., as described in U.S. Pat. No. 4,469,863; and alkylphosphotriesters (in which the charged oxygen moiety is alkylated as described in U.S. Pat. No. 5,023,243 and European Patent No. 092,574) can be prepared by automated solid  
30 phase synthesis using commercially available reagents. Methods for making other DNA backbone modifications and substitutions have been described. Uhlmann E and Peyman A (1990) *Chem Rev* 90:544; Goodchild J (1990) *Bioconjugate Chem* 1:165.



- 35 -

Other sources of immunostimulatory nucleic acids useful according to the invention include standard viral and bacterial vectors, many of which are commercially available. In its broadest sense, a "vector" is any nucleic acid material which is ordinarily used to deliver and facilitate the transfer of nucleic acids to cells. The vector as used herein may be an empty  
 5 vector or a vector carrying a gene which can be expressed. In the case when the vector is carrying a gene the vector generally transports the gene to the target cells with reduced degradation relative to the extent of degradation that would result in the absence of the vector. In this case the vector optionally includes gene expression sequences to enhance expression of the gene in target cells such as immune cells, but it is not required that the gene  
 10 be expressed in the cell.

Nucleic acid-binding fragments of TLRs are believed to include the extracytoplasmic (extracellular) domain or subportions thereof, such as those which include at least an MBD motif, a CXXC motif, or both an MBD motif and a CXXC motif.

Both mouse and human TLR9 have an N-terminal extension of approximately 180  
 15 amino acids compared to other TLRs. An insertion also occurs at amino acids 253-268, which is not found in TLRs 1-6 but is present in human TLR7 and human TLR8. This insert has two CXXC motifs which participate in forming a CXXC domain. The CXXC domain resembles a zinc finger motif and is found in DNA-binding proteins and in certain specific CpG binding proteins, e.g., methyl-CpG binding protein-1 (MBD-1). Fujita N et al. (2000)  
 20 *Mol Cell Biol* 20:5107-18. Both human and mouse TLR9 CXXC domains occur at aa 253-268:

CXXC motif:	GNCXXCXXXXXXXXXXCXXC	SEQ ID NO:62
Human TLR9:	GNCRRCDHAPNPCMEC	SEQ ID NO:63
25 Murine TLR9:	GNCRRCDHAPNPCMIC	SEQ ID NO:64

An additional motif believed to be involved in CpG binding is the MBD motif, also found in MBD-1, listed below as SEQ ID NO:53. Fujita, N et al.(2000) *Mol Cell Biol* 20:5107-18; Ohki I et al. (1999) *EMBO J* 18:6653-61. Amino acids 524-554 of hTLR9 and  
 30 aa 525-555 of mTLR9 correspond to the MBD motif of MBD-1 as shown:

MBD motif:

- 36 -

	MBD-1	R-XXXXXXX-R-X-D-X-Y-XXXXXXXXX-R-S-XXXXXX-Y	SEQ ID NO:65
	hTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXX-R-L-XXXXXX-Y	SEQ ID NO:66
	mTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXX-Q-L-XXXXXX-Y	SEQ ID NO:67
5	hTLR9	Q-VLDLSRN-K-L-D-L-Y-HEHSFTELP-R-L-EALDLS-Y	SEQ ID NO:68
	mTLR9	Q-VLDLSHN-K-L-D-L-Y-HWKSFSLEP-Q-L-QALDLS-Y	SEQ ID NO:69

Although the signaling functions of MBD-1 and TLR9 are quite different, the core D-X-Y is conserved and is believed to be involved in CpG binding.

10 According to another aspect of the invention, a screening method is provided for identifying an immunostimulatory compound. The method according to this aspect of the invention involves contacting a functional TLR9 with a test compound; detecting presence or absence of a response mediated by a TLR9 signal transduction pathway in the presence of the test compound arising as a result of an interaction between the functional TLR9 and the test  
15 compound; and determining the test compound is an immunostimulatory compound when the presence of a response mediated by the TLR9 signal transduction pathway is detected.

An immunostimulatory compound is a natural or synthetic compound that is capable of inducing an immune response when contacted with an immune cell. A TLR9 ligand that is an immunostimulatory compound is a natural or synthetic compound that is capable of  
20 inducing an immune response when contacted with an immune cell that expresses TLR9. A TLR9 ligand that is an immunostimulatory compound is also a natural or synthetic compound that is capable of inducing a TLR/IL-1R signal transduction pathway when contacted with a TLR9. Immunostimulatory compounds include but are not limited to immunostimulatory  
25 molecule, polynucleotide or oligonucleotide, a polypeptide or oligopeptide, a lipid or lipopolysaccharide, a small molecule.

A basis for certain of the screening assays is the presence of a functional TLR9 in a cell. The functional TLR9 in some instances is naturally expressed by a cell. In other instances, expression of the functional TLR9 can involve introduction or reconstitution of a  
30 species-specific TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact with an

- 37 -

immunostimulatory nucleic acid. In yet other instances, expression of the functional TLR9 can involve introduction of a chimeric or modified TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact  
5 with an immunostimulatory nucleic acid. Examples of cell lines lacking TLR9 or immunostimulatory nucleic acid responsiveness include, but are not limited to, 293 fibroblasts (ATCC CRL-1573), MonoMac-6, THP-1, U937, CHO, and any TLR9 knock-out. The introduction of the species-specific, chimeric or modified TLR9 into the cell or cell line is preferably accomplished by transient or stable transfection of the cell or cell line with a  
10 TLR9-encoding nucleic acid sequence operatively linked to a gene expression sequence (as described above). Methods for transient and for stable transfection of a cell are well known in the art.

The screening assays can have any of a number of possible readout systems based upon either TLR/IL-1R signaling pathway or other assays useful for assessing response to  
15 immunostimulatory nucleic acids. It has been reported that immune cell activation by CpG immunostimulatory sequences is dependent in some way on endosomal processing.

In certain embodiments, the readout for the screening assay is based on the use of native genes or, alternatively, cotransfected or otherwise co-introduced reporter gene constructs which are responsive to the TLR/IL-1R signal transduction pathway involving  
20 MyD88, TRAF, p38, and/or ERK. Häcker H et al. (1999) *EMBO J* 18:6973-6982. These pathways activate kinases including  $\kappa$ B kinase complex and c-Jun N-terminal kinases. Thus reporter genes and reporter gene constructs particularly useful for the assays can include a reporter gene operatively linked to a promoter sensitive to NF- $\kappa$ B. Examples of such promoters include, without limitation, those for NF- $\kappa$ B, IL-1 $\beta$ , IL-6, IL-8, IL-12 p40, CD80,  
25 CD86, and TNF- $\alpha$ . The reporter gene operatively linked to the TLR-sensitive promoter can include, without limitation, an enzyme (e.g., luciferase, alkaline phosphatase,  $\beta$ -galactosidase, chloramphenicol acetyltransferase (CAT), etc.), a bioluminescence marker (e.g., green-fluorescent protein (GFP, U.S. Pat. No. 5,491,084), blue fluorescent protein, etc.), a surface-expressed molecule (e.g., CD25), and a secreted molecule (e.g., IL-8, IL-12 p40, TNF- $\alpha$ ). In  
30 certain embodiments the reporter is selected from IL-8, TNF- $\alpha$ , NF- $\kappa$ B-luciferase (NF- $\kappa$ B-luc; Häcker H et al. (1999) *EMBO J* 18:6973-6982), IL-12 p40-luc (Murphy TL et al. (1995)

- 38 -

*Mol Cell Biol* 15:5258-5267), and TNF-luc (Häcker H et al. (1999) *EMBO J* 18:6973-6982). At least one of these reporter constructs (NF- $\kappa$ B-luc) is commercially available (Stratagene, La Jolla, CA). In assays relying on enzyme activity readout, substrate can be supplied as part of the assay, and detection can involve measurement of chemiluminescence, fluorescence, color development, incorporation of radioactive label, drug resistance, or other marker of enzyme activity. For assays relying on surface expression of a molecule, detection can be accomplished using FACS analysis or functional assays. Secreted molecules can be assayed using enzyme-linked immunosorbent assay (ELISA) or bioassays. Many such readout systems are well known in the art and are commercially available.

According to one embodiment of this method, comparison can be made to a reference immunostimulatory nucleic acid. The reference immunostimulatory nucleic acid may be any suitably selected immunostimulatory nucleic acid, including a CpG nucleic acid. In certain embodiments the screening method is performed using a plurality of test nucleic acids. In certain embodiments comparison of test and reference responses is based on comparison of quantitative measurements of responses in each instance.

In another aspect the invention provides a screening method for identifying species specificity of an immunostimulatory nucleic acid. The method involves contacting a TLR9 of a first species with a test immunostimulatory nucleic acid; contacting a TLR9 of a second species with the test immunostimulatory nucleic acid; measuring a response mediated by a TLR signal transduction pathway associated with the contacting the TLR9 of the first species with the test immunostimulatory nucleic acid; measuring a response mediated by the TLR signal transduction pathway associated with the contacting the TLR9 of the second species with the test immunostimulatory nucleic acid; and comparing the two responses. The TLR9 may be expressed by a cell or it may be part of a cell-free system. The TLR9 may be part of a complex, with either another TLR or with another protein, e.g., MyD88, IRAK, TRAF, I $\kappa$ B, NF- $\kappa$ B, or functional homologues and derivatives thereof. Thus for example a given ODN can be tested against a panel of human fibroblast 293 fibroblast cells transfected with TLR9 from various species and optionally cotransfected with a reporter construct sensitive to TLR/IL-1R activation pathways. Thus in another aspect, the invention provides a method for screening species selectivity with respect to a given nucleic acid sequence.

Test compounds can include but are not limited to peptide nucleic acids (PNAs), antibodies, polypeptides, carbohydrates, lipids, hormones, and small molecules. Test

- 39 -

compounds can further include variants of a reference immunostimulatory nucleic acid incorporating any one or combination of the substitutions described above. Test compounds can be generated as members of a combinatorial library of compounds.

In preferred embodiments, the screening methods can be performed on a large scale and with high throughput by incorporating, e.g., an array-based assay system and at least one automated or semi-automated step. For example, the assays can be set up using multiple-well plates in which cells are dispensed in individual wells and reagents are added in a systematic manner using a multiwell delivery device suited to the geometry of the multiwell plate. Manual and robotic multiwell delivery devices suitable for use in a high throughput screening assay are well known by those skilled in the art. Each well or array element can be mapped in a one-to-one manner to a particular test condition, such as the test compound. Readouts can also be performed in this multiwell array, preferably using a multiwell plate reader device or the like. Examples of such devices are well known in the art and are available through commercial sources. Sample and reagent handling can be automated to further enhance the throughput capacity of the screening assay, such that dozens, hundreds, thousands, or even millions of parallel assays can be performed in a day or in a week. Fully robotic systems are known in the art for applications such as generation and analysis of combinatorial libraries of synthetic compounds. See, for example, U.S. Pat. Nos. 5,443,791 and 5,708,158.

The following examples are provided for illustrative purposes and are not meant to be limiting in any way.

### Examples

Example 1. Cloning and Sequencing of Rat, Porcine, Bovine, Equine, Ovine, Canine, and Feline TLR9

*Cells and Tissues.* Lymphoid tissues, primarily spleen or blood mononuclear cells (PBMC) from five mammalian species were collected: mouse, pig, bovine, rat and horse. Spleen samples were collected in RNeasy<sup>TM</sup> (Ambion<sup>®</sup>, Austin, TX, USA), stabilized at 4°C overnight and stored at -70°C. Blood samples were centrifuged at 500 x g for 25 min at room temperature and the buffy coat, containing enriched PBMC, was then removed and stored at -70°C. The mouse specimen was used as a comparative positive control.

- 40 -

*First-strand cDNA synthesis.* Total RNA from the spleen and PBMC samples was isolated using a monophasic solution of phenol and guanidine isothiocyanate: TRIzol™ reagent (GIBCO BRL®, Burlington, ON, Canada) according to the manufacturer's instructions. First-strand cDNA was synthesized from the total RNA using  
5 SUPERScript™ II reverse transcriptase (GIBCO BRL®, Burlington, ON, Canada). Approximately 3 µg of total RNA was added to 50 pmoles of oligo(dT) primer [poly T<sub>(18)</sub>]; the mixture was heated to 70°C for 10 min and subsequently chilled on ice. The following was added to the cooled reaction mixture: 1 µl of mixed dNTP stock containing 10 mM each dATP, dCTP, dGTP and dTTP (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) at  
10 neutral pH, 1X first strand buffer (50 mM Tris-HCl pH 8.3/ 75 mM KCl/ 3 mM MgCl<sub>2</sub>) and 2 µl of 0.1 M DTT. The mixture was subsequently heated to 42°C for 2 min, followed by addition of 200 units of SUPERScript™ II reverse transcriptase. The reaction was carried out at 42°C for 50 min, followed by 70°C for 15 min. The first-strand cDNA was used as the template for subsequent polymerase chain reaction (PCR) amplifications.

15 *PCR amplification.* TLR9 gene was PCR amplified from each of the above-mentioned species using primers designed from known mouse and human TLR9 sequence in Genbank: Accession AF314224 and AF259262, respectively. The primers were designed using the primer design software, Clone Manager 5 (Scientific and Educational Software, Durham, NC, USA). TLR9 gene-specific primers used were:

20 forward primer 5'-ACCTTGCCTGCCTTCCTACCCTGTGA-3' (SEQ ID NO:37) and reverse primer 5'-GTCCGTGTGGGCCAGCACAAA-3' (SEQ ID NO:38).

The 2.7 Kbp fragment was PCR amplified using Advantage® 2 DNA polymerase mix (BD Biosciences Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. PCR reaction volumes of 25 µl contained 15 pmoles of each primer, 0.2 mM of dNTP mix  
25 and 1 µl of reverse transcription reaction. PCR amplification was conducted by initial denaturation at 94°C for 1 min followed by 30 cycles of 94°C denaturation (15 sec), 65°C annealing (45 sec) and 72°C extensions (2 min), with a final extension at 72°C for 5 min.

*Cloning and sequencing.* The PCR amplified fragment was treated with 500 units of T4 DNA polymerase (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) for 15 min  
30 at room temperature prior to cleaning the reaction with QIAquick PCR purification kit (QIAGEN Inc., Mississauga, ON, Canada). The fragment was then ligated to pZerO™ - 2

- 41 -

vector (Invitrogen™ Life Technologies, Burlington, ON, Canada), treated with *Eco RV* restriction enzyme, using T4 DNA Ligase (GIBCO BRL®, Burlington, ON, Canada). *E. coli* TOP 10 chemically competent cells (Invitrogen™ Life Technologies, Burlington, ON, Canada) were used to transform ligated products. Plasmids containing the 2.7 Kbp fragment were sequenced using an automated DNA sequencer, CEQ™ 2000XL DNA analysis system (Beckman Coulter Inc., Fullerton, CA, USA).

Sequences of the 2.7 Kbp fragment were derived from three clones of each species selected from independent PCR reactions to account for errors that may have been incurred during the PCR amplifications and to confirm the sequence data.

Nucleotide sequences of the rat, porcine, bovine, equine, ovine, canine, and feline TLR9 were extended and completed using standard 5' and 3' RACE PCR and primers designed using the sequences obtained from the 2.7 Kbp fragments.

**Results.** Nucleotide sequences of rat, porcine, bovine, equine, canine, and feline TLR9 cDNA obtained by the methods above are provided as SEQ ID NOs 3, 7, 11, 15, 19, 23, and 27, respectively. Deduced amino acid sequences are provided as SEQ ID NOs 1, 5, 9, 13, 17, 21, and 25, respectively. Deduced amino acid sequences of full-length murine and human TLR9 are provided as SEQ ID NOs 29 and 33, respectively.

#### Example 2. Comparison of Aligned Sequences for TLR9 from Various Mammalian Species.

Multiple sequence alignment of deduced amino acid sequences for feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 polypeptides was performed using Clustal W 1.82 (see, for example, [www.cmbi.kun.nl/bioinf/tools/clustalw.shtml](http://www.cmbi.kun.nl/bioinf/tools/clustalw.shtml)). In addition, paired sequence alignment of deduced amino acid sequences for murine and human TLR9 polypeptides was performed using Clustal W 1.82. The results of the multiple sequence alignment are presented in Figure 1. As will be appreciated from Figure 1, certain amino acids are highly conserved across all species examined. Similarly, certain amino acids differ only by conservative amino acid substitutions among the various species. In addition, it is evident that certain amino acids which are conserved between murine and human TLR9 are not conserved in other species. Furthermore, Figure 1 also indicates that certain amino acids are highly divergent across various species. The information provided by the comparison of multiple species adds significantly to the information available by comparison between only murine and human TLR9 sequences.

- 42 -

The putative transmembrane regions of the TLR9 polypeptides are indicated in boxes in Figure 1. Sequence upstream of each transmembrane region is extracellular domain and is believed to include sequence primarily responsible for binding to TLR9 ligands, including CpG DNA. The extracellular domains of feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 correspond to amino acids numbered 1-820, 1-822, 1-818, 1-821, 1-818, 1-819, 1-820, 1-820, and 1-821, respectively, as shown in Figure 1.

Figure 2 presents an evolutionary relatedness tree for six TLR9 polypeptides examined. The cladogram in Figure 2 was prepared using Clustal W (see above). As can be appreciated from this figure, murine and human TLR9 are nearly the most divergent TLR9s in this group. Surprisingly, human and horse TLR9 appear relatively closely related.

### Example 3. Reconstitution of TLR9 Signaling in 293 Fibroblasts.

Mouse TLR9 cDNA (SEQ ID NO:31) and human TLR9 cDNA (SEQ ID NO:35) in pT-Adv vector (from Clontech) were individually cloned into the expression vector pcDNA3.1(-) from Invitrogen using the EcoRI site. Utilizing a "gain of function" assay it was possible to reconstitute human TLR9 (hTLR9) and murine TLR9 (mTLR9) signaling in CpG-DNA non-responsive human 293 fibroblasts (ATCC, CRL-1573). The expression vectors mentioned above were transfected into 293 fibroblast cells using the calcium phosphate method.

Since NF- $\kappa$ B activation is central to the IL-1/TLR signal transduction pathway (Medzhitov R et al. (1998) *Mol Cell* 2:253-258; Muzio M et al. (1998) *J Exp Med* 187:2097-101), cells were transfected with hTLR9 or co-transfected with hTLR9 and an NF- $\kappa$ B-driven luciferase reporter construct. Human fibroblast 293 cells were transiently transfected with hTLR9 and a six-times NF- $\kappa$ B-luciferase reporter plasmid (NF- $\kappa$ B-luc) or with hTLR9 alone. After stimulus with CpG-ODN (2006, 2 $\mu$ M, TCGTCGTTTTGTCGTTTTGTCGTT, SEQ ID NO:58), GpC-ODN (2006-GC, 2 $\mu$ M, TGCTGCTTTTGTGCTTTTGTGCTT, SEQ ID NO:59), LPS (100 ng/ml) or media, NF- $\kappa$ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results representative of three independent experiments showed that cells expressing hTLR9 responded to CpG-DNA but not to LPS.

Independently, human fibroblast 293 cells were transiently transfected with mTLR9 and the NF- $\kappa$ B-luc construct or with mTLR9 alone. After stimulation with CpG-ODN (1668, 2 $\mu$ M; TCCATGACGTTCCCTGATGCT, SEQ ID NO:60), GpC-ODN (1668-GC, 2 $\mu$ M;



- 43 -

TCCATGAGCTTCCTGATGCT, SEQ ID NO:61), LPS (100 ng/ml) or media, NF- $\kappa$ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results showed that expression of TLR9 (human or mouse) in 293 cells results in a gain of function for CpG-DNA stimulation.

5 To generate stable clones expressing human TLR9, murine TLR9, or either TLR9 with the NF- $\kappa$ B-luc reporter plasmid, 293 cells were transfected in 10 cm plates ( $2 \times 10^6$  cells/plate) with 16  $\mu$ g of DNA and selected with 0.7 mg/ml G418 (PAA Laboratories GmbH, Cölbe, Germany). Clones were tested for TLR9 expression by RT-PCR. The clones were also screened for IL-8 production or NF- $\kappa$ B-luciferase activity after stimulation with  
10 ODN. Four different types of clones were generated.

293-hTLR9-luc:	expressing human TLR9 and 6-fold NF- $\kappa$ B-luciferase reporter
293-mTLR9-luc:	expressing murine TLR9 and 6-fold NF- $\kappa$ B-luciferase reporter
293-hTLR9:	expressing human TLR9
15 293-mTLR9:	expressing murine TLR9

Results indicated that stable clones also responded to CpG-ODN.

Example 4. Similar ODN Sequence Specificity of TLR9 of Human and Equine TLR9.

20  $3 \times 10^6$  293T cells were electroporated with 5  $\mu$ g NF- $\kappa$ B-luc plasmid and 5  $\mu$ g of either horse TLR9-pcDNA3.1 plasmid or human TLR9-pcDNA3.1 plasmid at 200V, 975  $\mu$ F. After the electroporation the cells were plated in 96-well cell culture plates at  $2.5 \times 10^4$  cells per well and grown overnight at 37°C. The cells were stimulated with the indicated concentration of ODN for 16h, after which the supernatant was removed and the cells lysed in lysis buffer and  
25 frozen for at least 2 hours at -80°C. Luciferase activity was measured by adding Luciferase Assay substrate from Promega. Values are given as fold specific induction over non-stimulated control. Results are shown in Figure 3.

As shown in Figure 3, ODN 2006 (TCGTCGTTTTGTCGTTTTGTCGTT; SEQ ID NO:58) has a strong specificity for human TLR9. ODN 1982  
30 (TCCAGGACTTCTCTCAGGTT; SEQ ID NO:70) was the negative control ODN. ODN 5890 (TCCATGACGTTTTTGTATGTT; SEQ ID NO:39) has a strong specificity for mouse

- 44 -

TLR9. This experiment demonstrates the similarity of horse TLR9 to human TLR9 in binding specificity, a result predicted by the evolutionary relatedness of horse TLR9 to human TLR9. Mouse TLR9 is more distant from horse TLR9 and human TLR9 in sequence homology, and ODN 5890 was not detected by either human or horse TLR9.

5

Example 5. Non-human, Non-murine Native Mammalian TLR9 Useful in Screening for Human-Preferred CpG DNA.

Native rat, porcine, bovine, equine, and ovine TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Rat, porcine, bovine, equine, or ovine TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

20 Example 6. Chimeric TLR9 Useful in Screening for Human-Preferred CpG DNA.

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

30

Example 7. Chimeric TLR9 Responsive to Both Human-Preferred and Murine-Preferred CpG DNA.

- 45 -

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006) and also screened for binding or TLR9 signaling activity when contacted with murine-preferred CpG DNA (ODN 1668). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in each of these assays are then used as the basis for screening for additional human-preferred CpG DNA and for screening for additional murine-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA or candidate murine-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA. Candidate murine-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as murine-preferred CpG DNA.

### Equivalents

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by examples provided, since the examples are intended as a single illustration of one aspect of the invention and other functionally equivalent embodiments are within the scope of the invention. Various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims. The advantages of the invention are not necessarily encompassed by each embodiment of the invention.

All references, patents and patent publications that are recited in this application are incorporated in their entirety herein by reference.

We claim:

- 46 -

**Claims**

1. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.

5

2. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.

3. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.

10

4. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.

15

5. A vector comprising the nucleic acid of any of claims 3-4.

6. A cell comprising the vector of claim 5.

20

7. An antibody or fragment thereof that binds specifically to the polypeptide of any of claims 1-2.

8. A method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the first species, comprising:  
aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species;  
generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the

25

30

- 47 -

TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

10 9. A method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9, comprising:

aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a CpG DNA optimized for murine TLR9;

generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids.

25

10. The method according to claim 9, performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight, said weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred CpG DNA).

30

- 48 -

11. An isolated polypeptide comprising an amino acid sequence identical to SEQ ID NO:30 except for substitution of at least one key amino acid identified according to the method of any of claims 9 or 10.

5 12. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide according to claim 11.

13. A vector comprising the nucleic acid of claim 12.

10 14. A cell comprising the vector of claim 13.

15. An antibody that binds specifically to the polypeptide of claim 14.

16. A screening method to identify a TLR9 ligand, comprising:  
15 contacting a polypeptide according to any of claims 1, 2, or 11 with a candidate TLR9 ligand;  
measuring a signal in response to the contacting; and  
identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling.

20 17. The method of claim 16, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

25 18. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B.

19. The method of claim 17, wherein the candidate TLR9 ligand is an immunostimulatory nucleic acid.

30 20. The method of claim 19, wherein the immunostimulatory nucleic acid is CpG DNA.

- 49 -

21. A screening method to identify species-specific CpG-motif preference of an isolated polypeptide of claim 2 or claim 11, comprising:

contacting an isolated polypeptide of claim 2 or claim 11 with a CpG DNA comprising a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG;

measuring a signal in response to the contacting; and

identifying a species-specific CpG-motif preference when the signal in response to the contacting is consistent with TLR9 signaling.

22. The method of claim 21, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

23. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B.

24. The method of claim 21, wherein the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

20	TCCATGACGTTTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTTTGATGTT	(SEQ ID NO:41),
	TCCATTACGTTTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTTTGATGTT	(SEQ ID NO:43),
25	TCCATGCCGTTTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTTTGATGTT	(SEQ ID NO:46),
	TCCATGAAGTTTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTTTGATGTT	(SEQ ID NO:48),
30	TCCATGACATTTTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTTTGATGTT	(SEQ ID NO:50),
	TCCATGACTTTTTTGATGTT	(SEQ ID NO:51),
	TCCATGACGCTTTTGATGTT	(SEQ ID NO:52),
	TCCATGACGATTTTGATGTT	(SEQ ID NO:53),
35	TCCATGACGGTTTTGATGTT	(SEQ ID NO:54),
	TCCATGACGTCTTTGATGTT	(SEQ ID NO:55),
	TCCATGACGTATTTGATGTT	(SEQ ID NO:56), and
	TCCATGACGTGTTTGATGTT	(SEQ ID NO:57).

Figure 1  
(1/3)

```
feline      MGPCHGALHPLSLLVQAAALAVALAQGTLPAPFLPCELQPHGLVNCNWLFLKSVPHFSAAA 60
canine      MGPCRGALHPLSLLVQAAALALALAQGTLPAPFLPCELQPHGLVNCNWLFLKSVPRFSAAA 60
bovine      MGP-YCAPHPLSLLVQAAALAAALAEGTLPAPFLPCELQPHGQVDCNWLFLKSVPHFSAGA 59
mouse       MGP-YCAPHPLSLLVQAAALAAALAEGTLPAPFLPCELQPHGQVDCNWLFLKSVPHFSAGA 59
ovine       MGP-YCAPHPLSLLVQAAALAAALAEGTLPAPFLPCELQPHGQVDCNWLFLKSVPRFSAGA 59
porcine     MGP-RCTLHPLSLLVQVTAALAAALAEGTLPAPFLPCELQPHGLVNCNWLFLKSVPHFSAAA 59
horse       MGPCHGALQPLSLLVQAAMLAVALAAGTLPAPFLPCELQPHGLVNCNWLFLKSVPHFSAAA 60
human       MGFCRSALHPLSLLVQAIALMLATLALGTLPAPFLPCELQPHGLVNCNWLFLKSVPHFSMAA 60
rat         MVLCRRTLHPLSLLVQAALAEALALGTLPAPFLPCELKPHGLVDCNWLFLKSVPHFSAAE 60
*           : :*****. ** : * * * *.*****: : * *:*****:***

feline      PRGNVTSLSLSYNSRIHHLHDSDFVHLSSRLRLNLKWNCPASLSPMHFPCMTIEPHTFL 120
canine      PRGNVTSLSLSYNSRIHHLHDYDFVHFVHLRLNLKWNCPASLSPMHFPCMTIEPNTFL 120
bovine      PRANVTSLSLSISNRIHHLHDSDFVHLSNLRLNLKWNCPAGLSPMHFPCMTIEPNTFL 119
mouse       PRANVTSLSLSISNRIHHLHDSDFVHLSNLRLNLKWNCPAGLSPMHFPCMTIEPNTFL 119
ovine       PRANVTSLSLSISNRIHHLHDSDFVHLSNLRLNLKWNCPAGLSPMHFPCMTIEPNTFL 119
porcine     PRANVTSLSLSISNRIHHLHDSDFVHLSSRLTLNLKWNCPAGLSPMHFPCMTIEPNTFL 119
horse       PRDNVTSLSLSISNRIHHLHDSDFVHLSSRLTLNLKWNCPAGLSPMHFPCMTIEPNTFL 120
human       PRGNVTSLSLSISNRIHHLHDSDFVHLPSLRLNLKWNCPVGLSPMHFPCMTIEPSTFL 120
rat         PRSNITSLSLIANRIHHLHDLDFVHLPNVRQLNLKWNCPVGLSPMHFPCMTIEPSTFL 120
** *:***** :*****: **.: : *****. *****:***** **

feline      AVPTLEELNLSYNSITVPALPSSLVSLSLRTNLIIVLDPANLAGLSLRFLELDGNCYY 180
canine      AVPTLEELNLSYNSITVPALPSSLVSLSLRTNLIIVLDPATLAGLYALRFLELDGNCYY 180
bovine      AVPTLEELNLSYNGITVPALPSSLVSLSLSHTSILVLGPTHFTGLHALRFLYMDGNCYY 179
mouse       AVPTLEELNLSYNGITVPALPSSLVSLSLSHTSILVLGPTHFTGLHALRFLYMDGNCYY 179
ovine       AVPTLEELNLSYNGITVPALPSSLVSLSLSHTSILVLGPTHFTGLHALRFLYMDGNCYY 179
porcine     AVPTLEELNLSYNSITVPALPSSLVSLSLRTNLIIVLDPHTLGLHALRFLYMDGNCYY 179
horse       AVPTLEELNLSYNGITVPALPSSLVSLSLRTNLIIVLDPHTLGLHALRFLYMDGNCYY 180
human       AVPTLEELNLSYNNITVPALPKSLISLSHTNLIIMLDSASLAGLHALRFLYMDGNCYY 180
rat         AMRMLEELNLSYNGITVPRLPSSLTNLSHTNLIIVLDASSLAGLSLRLVFMGNCYY 180
*: ** :*****. * *** **.* * *:***. * *.: :*:*** :*:*****

feline      KNPCQALQVAPGALLGLGNLTHLSLKYNLTA VPRGLPPSLEYLLSYNHIITLAPEDL 240
canine      KNPCQALQVAPGALLGLGNLTHLSLKYNLTVVPRGLPPSLEYLLSYNHIITLAPEDL 240
bovine      MNPCPRALEVAPGALLGLGNLTHLSLKYNLTVVPRGLPPSLDTLLSYNHIVTLAPEDL 239
mouse       MNPCPRALEVAPGALLGLGNLTHLSLKYNLTVVPRGLPPSLDTLLSYNHIVTLAPEDL 239
ovine       KNPCQALEVAPGALLGLGNLTHLSLKYNLTVVPRGLPPSLDTLLSYNHIVTLAPEDL 239
porcine     KNPCQALEVAPGALLGLGNLTHLSLKYNLTVVPRGLPPSLEYLLSYNHIITLAPEDL 240
horse       KNPCQALEVAPGALLGLGNLTHLSLKYNLTVVPRGLPPSLEYLLSYNHIITLAPEDL 240
human       KNPCQALEVAPGALLGLGNLTHLSLKYNLTVVPRGLPPSLEYLLSYNHIITLAPEDL 240
rat         KNPCGAVNVTDAFLGLSNLTHLSLKYNLTVVPRGLPPSLEYLLSYNLIVKLGAEDL 240
*** *:***.***:***** ***** ** *:***: ***** *:***

feline      ANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLPDTFSLNHLLEGLVLKDSLSYLN 300
canine      ANLTALRVLDVGGNCRRCDHARNPCRECPKGFPHLPDTFSLNHLLEGLVLKDSLSYLD 300
bovine      ANLTALRVLDVGGNCRRCDHARNPCRECPKNFPHLPDTFSLNHLLEGLVLKDSLSYKLE 299
mouse       ANLTALRVLDVGGNCRRCDHARNPCRECPKNFPHLPDTFSLNHLLEGLVLKDSLSYKLE 299
ovine       ANLTALRVLDVGGNCRRCDHARNPCRECPKNFPHLPDTFSLNHLLEGLVLKDSLSYKLE 299
porcine     ANLTALRVLDVGGNCRRCDHARNPCRECPKDPHLPDTFSLNHLLEGLVLKDSLSYKLE 299
horse       ANLTALRVLDVGGNCRRCDHARNPCRECPKDPHLPDTFSLNHLLEGLVLKDSLSYKLE 300
human       ANLTALRVLDVGGNCRRCDHARNPCRECPKDPHLPDTFSLNHLLEGLVLKDSLSYKLE 300
rat         ANLTALRVLDVGGNCRRCDHARNPCRECPKDPHLPDTFSLNHLLEGLVLKDSLSYKLE 300
*****:*****: * * *: **.:** *:*****:***** **

feline      PRWFHALGNLMVLDLSENFLYDCITKTTFQGLAQRLRLNLSFNHKKVVSFAHLHLAPSF 360
canine      PRWFHGLGNLMVLDLSENFLYDCITKTTFQGLAQRLRLNLSFNHKKVVSFAHLHLAPSF 360
bovine      KDWFRGLGRLQVLDLSENFLYDYITKTTFQGLAQRLRLNLSFNHKKVVSFAHLHLAPSF 359
mouse       KDWFRGLGRLQVLDLSENFLYDYITKTTFQGLAQRLRLNLSFNHKKVVSFAHLHLAPSF 359
ovine       KDWFRGLGRLQVLDLSENFLYDYITKTTFQGLAQRLRLNLSFNHKKVVSFAHLHLAPSF 359
porcine     TRWFRGLDRLQVLDLSENFLYDCITKTTFQGLAQRLRLNLSFNHKKVVSFAHLHLAPSF 359
horse       PRWFRGLGNLTVLDLSENFLYDCITKTTFQGLAQRLRLNLSFNHKKVVSFAHLHLAPSF 360
human       ASWFRGLGNLTVLDLSENFLYKCTKTTFQGLAQRLRLNLSFNHKKVVSFAHLHLAPSF 360
rat         SKWFRGLGNLTVLDLSENFLYKCTKTTFQGLAQRLRLNLSFNHKKVVSFAHLHLAPSF 360
**:* * * *****. *.*. * *:*** *:***** *:***** **
```



**Figure 1**  
**(2/3)**

feline	GSLLSLQQLDMHGIFFRSLSETTLRSLVHLPLMQSLHLMQNFINQAQLSIFGAFFGLRYV	420
canine	GSLLSLQELDIHGIFFRSLSKTTLQSLAHLPMLORLHLQLNFIQAQLSIFGAFFGLRYV	420
bovine	GSLVSLEKLDMHGIFFRSLNTITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAFFSLLFV	419
mouse	GSIVSLEKLDMHGIFFRSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAFFSLLFV	419
ovine	GGLVSLEKLDMHGIFFRSLTNTTLRPLTQLPKLQSLSLQLNFINQAELSIFGAFFSLLFV	419
porcine	GHLRSLEKLDMHGIFFRSLSETTLQPLVLQPLMLQTLRLQMNFINQAQLSIFGAFFGLLYV	419
horse	GSLLSLQELDMHGIFFRSLSQKTLPQLARLPMLORLYLQMNFINQAQLGIKFDPGLRYI	420
human	GSLVALKEKLDMHGIFFRSLDETTLRLPRLMLOTLRLQMNFINQAQLGIFRAFPGLRYV	420
rat	KSLVSLQELNMNGIFFRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVSTFRALRFV	420
	* : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
feline	DLSDNRIISGAMELAAATGEVDG--GERVRLPSGDIALGPPTSPSEGFMPGCKTILNFTLD	478
canine	DLSDNRIISGAAPAAATGEVEADCGERVWPQSRODALGPGLTGPEAFMPSCRTLNFTLD	480
bovine	DLSDNRIISGAATPAALGEVDS--RVEVWLPRGLAPGPLDAVSSKDMPSCN-LNFTLD	476
mouse	DLSDNRIISGAATPAALGEVDS--RVEVWLPRGLAPGPLDAVSSKDMPSCN-LNFTLD	476
ovine	DLSDNRIISGAARPVAALGEVDS--GVEVWRWPRGLAPGPLAAVSAKDFMPSCN-LNFTLD	476
porcine	DLSDNRIISGAARPVAITREVDG--RERVWLPSRNLAAPRLDTRSEDFMPCNAKSFTLD	477
horse	DLSDNRIISGAEPVATTEVDG--GKKVWLTSRDLTTPGLDTPSSEDFMPCSKNLSTFLD	478
human	DLSDNRIISGASELTATMGEDG--GEKVWLQPGLAPAPVDTPSSEDFRPCNSTLNFTLD	478
rat	DLSNNRIISGPPTLSRVAPKAD-EAEKGVPWPASLTAPLSTPVSKNFMVRCKNLRFMTD	479
	*** : ***** . * : . . . : * : * : * : * : *	
feline	LRRNNLVTIQPEMFARLSRLQCILLSRNSISQAVNGSQFMPLTSLQVLDLSHNKLDLYHG	538
canine	LRRNNLVTVQPEMFVRLARLQCGLSHNSISQAVNGSQFVPLSNLRVLDLSHNKLDLYHG	540
bovine	LRRNNLVTIQPEMFTLRSLRLQCCLRLSHNSISQAVNGSQFVPLTLRVLDSLHNKLDLYHG	536
mouse	LRRNNLVTIQPEMFTLRSLRLQCCLRLSHNSISQAVNGSQFVPLTLRVLDSLHNKLDLYHG	536
ovine	LRRNNLVTIQPEMFTLRSLRLQCCLRLSHNSISQAVNGSQFVPLTLRVLDSLHNKLDLYHG	536
porcine	LRRNNLVTIQSEMFAQLSRLECLRSHNSISQAVNGSQFVPLTLRVLDSLHNKLDLYHG	537
horse	LRRNNLVTVQPEMAFQRSRLQCCLRLSHNSISQAVNGSQFVPLTSLQVLDLSHNKLDLYHG	538
human	LRRNNLVTVQPEMAFQRSRLQCCLRLSHNSISQAVNGSQFVPLTGQVLDLSHNKLDLYHE	538
rat	LRRNNQVTIKPEMFVNLSHLQCCLSLSHNCIAQAVNGSQFPLTLNLKVLDSLHNKLDLYHS	539
	***** * : * : * : * : * : * : * : * : * : * : * : * : *	
feline	RSFTELPRLEALDLSYNSQPFMSMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSA	598
canine	RSFTELPRLEALDLSYNSQPFMSMRGVGHNLSFVAQLPALRYLSLAHNGIHSRVSQQLRSA	600
bovine	RSFTELPQLEALDLSYNSQPFMSMQGVGHNLSFVAQLPSLRYSLAHNGIHSRVSQQLSSA	596
mouse	RSFTELPQLEALDLSYNSQPFMSMQGVGHNLSFVAQLPSLRYSLAHNGIHSRVSQQLSSA	596
ovine	RSFTELPQLEALDLSYNSQPFMSMQGVGHNLSFVAQLPSLRYSLAHNGIHSRVSQQLSSA	596
porcine	RSFTELPRLEALDLSYNSQPFMTMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSA	597
horse	RSFTELPRLEALDLSYNSQPFMSMRGVGHNLSFVAQLPTLRYSLAHNGIHSRVSQQLCST	598
human	HSFTELPRLEALDLSYNSQPFMGQGVGHNFSFVAHLRTLRLHLSLAHNNIHSQVSOQLCST	598
rat	KSFSELPLQALDLSYNSQPFMSQGIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYST	599
	: * : * : * : * : * : * : * : * : * : * : * : * : * : *	
feline	SIRALDFSGNALSIRMWAEGDLYLHFFRGLRSLVRLDLSQNRHLTLLPRTLNLPKSLRL	658
canine	SIRALDFSGNLTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNRHLTLLPRLDLNLPKSLRL	660
bovine	SIRALDFSNGNSLSQMWAEGLDYLCFFKGLRNLVQLDLSKNHLHTLLPRLDLNLPKSLRQL	656
mouse	SIRALDFSNGNSLSQMWAEGLDYLCFFKGLRNLVQLDLSKNHLHTLLPRLDLNLPKSLRQL	656
ovine	SIRALDFSNGNSLSQMWAEGLDYLCFFKGLRNLVQLDLSKNHLHTLLPRLDLNLPKSLRQL	656
porcine	SLCALDFSNDLSRMWAEGDLYLRFFQGLRSLVWL DLSQNLHTLLPRLDLNLPKSLKHL	657
horse	SLWALDFSNGNSQMWAEGLDYLRHFFQGLRSLIRLDLSQNRHLTLLPCTLGNLPKSLQLL	658
human	SIRALDFSNGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNRHLTLLPQTIRNLNPKSLQVL	658
rat	SVEYLDIFSNGVGWMDEEDLYLYFFQDLRSLIHLDLSQNKHLILRPQNLNYPKSLTKL	659
	* : ***** : : * * * * * : * : * : * : * : * : * : * : *	
feline	RLRDNYLAFFNWSSLVLLPRLEALDLAGNQLKALSNGSLPNGTQLQRDLSSNSISFVAS	718
canine	RLRDNYLAFFNWSSLALLPKLEALDLAGNQLKALSNGSLPNGTQLQRDLSSNSIGFVVP	720
bovine	RLRDNNLAFFNWSSLTVLPRLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIP	716
mouse	RLRDNNLAFFNWSSLTVLPRLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIP	716
ovine	RLRDNNLAFFNWSSLTVLPQLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIP	716
porcine	HRLDNNLAFFNWSSLTLLPKLETLDLAGNQLKALSNGSLPSGTQLRRDLSSNSIGFVNP	717
horse	RLRDNYLAFFNWSSLTLLPNLETLDLAGNQLKALSNGSLPSGTQLQRDLVSRNSIIFVVP	718
human	RLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRDLVSCNSISFVAP	718
rat	SFRDNLHLSFNWSSLAFPLNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVEVVP	719
	. * * * * * * : * * * * * * : * * * * * * * : * * * * * * *	

feline	SFFALATRLRELNLNSANALKTVEPSWFGSLAGTLKVLDDVTGNPLHCACGAAFVDFLLEQV	778
canine	SFFALAVRLRELNLNSANALKTVEPSWFGSLAGALKVLDDVTANPLHCACGATFVDLFLEQV	780
bovine	GFFVRATRLIELNLNSANALKTVDPSPWFGSLAGTLKILDVSANPLHCACGAAFVDFLLERQ	776
mouse	GFFVRATRLIELNLNSANALKTVDPSPWFGSLAGTLKILDVSANPLHCACGAAFVDFLLERQ	776
ovine	GFFVLANKLKELNLSANALKTVDPFWFGRLTETLNLILDVSANPLHCACGAAFVDFLLEMQ	776
porcine	GFFALAKQLEELNLNSANALKTVEPSWFGSMVGNLKVLDDVSANPLHCACGATFVGFLLEQV	777
horse	GFFALATRLRELNLNSANALRTEEPSWFGFLAGSLVLDVSANPLHCACGAAFVDFLLQVQ	778
human	GFFSKAKELRELNLNSANALKTVDSHWFGLASALQILDDVSANPLHCACGAAFMDFLLEQV	778
rat	AFFALVELKVNLSHNILKTVDRSWFGPIVMNLTVDSSNPLHCACGAAPFDLLLEQV	779
	*.* * . * :**** * . * : ** : . * :**** :*****.*.:**:	
feline	AAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCCFGLSLLTVALGLAVPMLHHI	838
canine	AAVPGLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWSVCFSLSLLAVALSLAVPMLHQI	840
bovine	EAVPGLSRRTVCGSPGQLQGRSIFTQDLRLCLDETSLSDCFGLSLLMVALGLAVPMLHHI	836
mouse	EAVPGLSRRTVCGSPGQLQGRSIFTQDLRLCLDETSLSDCFGLSLLMVALGLAVPMLHHI	836
ovine	AAVPGLSRRTVCGSPGQLQGRSIFAQDLRLCLDETSLSDCFGLSLLMVALGLAVPMLHHI	836
porcine	AAVPGLPSRVKCGSPGQLQGHISIFAQDLRLCLDETSLSWNCFCISLLAMALGLVVPMLHHI	837
horse	AAVPGLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFCISLLLVVALGLAMPMLHHI	838
human	AAVPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCCFGLSLLAVALGLGVPMHLHI	838
rat	TKVPEGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCCFGLSLLAVAVGTVPPLLQHI	839
	****. *.**** ***** **.*****. ** **.**** :*. :*:***:*	
feline	CGDWLWYCFHLCLAWLPRRGR--RGADALPYDAFVVFDKAQSADADVYNELRVLEER	896
canine	CGDWLWYCFHLCLAWLPRRGR--RGVDALAYDAFVVFDKAQSSVADADVYNELRVQLEER	898
bovine	CGDWLWYCFHLCLLAHLPRRRQ--RGEDTLLYDAVVVFDDKVQSAVADADVYNELRVQLEER	894
mouse	CGDWLWYCFHLCLLAHLPRRRQ--RGEDTLLYDAVVVFDDKVQSAVADADVYNELRVQLEER	894
ovine	CGDWLWYCFHLCLLAHLPRRRQ--RGEDTLLYDAFVVFDDKAQSAVADADVYNELRVQLEER	894
porcine	CGDWLWYCFHLCLAWLPHRGR--RGADALFYDAFVVFDKAQSAVADADVYNELRVQLEER	895
horse	CGDWLWYCFHLGLAWLPRRGRQ--RGADALSYPDAFVVFDKAQSAVADADVYNELRVLEER	896
human	CGDWLWYCFHLCLAWLPWRGRSGRDEDALPYDAFVVFDKQTSADADVYNELRGQLEEC	898
rat	CGDWDVWYCFHLCLAWLP LLTRGR-RSAQALPYDAFVVFDKAQSAVADADVYNELRVLEER	898
	****.****** ** ** * . :* ***.*****.*:***** :***	
feline	RGRRALRLCLEERDWLP GKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQQRL	956
canine	RGRRALRLCLEERDWVP GKTLFENLWASVYSSRKTLFVLARTDRVSGLLRASFLLAQQRL	958
bovine	RGRRALRLCLEERDWLP GKTLFENLWASVYSSRKTMFVLDDHTDRVSGLLRASFLLAQQRL	954
mouse	RGRRALRLCLEERDWLP GKTLFENLWASVYSSRKTMFVLDDHTDRVSGLLRASFLLAQQRL	954
ovine	RGRRALRLCLEERDWLP GKTLFENLWASVYSSRKTMFVLDDHTDRVSGLLRASFLLAQQRL	954
porcine	RGRRALRLCLEERDWLP GKTLFENLWASVYSSRKTLFVLAHTDRVSGLLRASFLLAQQRL	955
horse	RGRRALRLCLEERDWLP GKTLFENLWASVYSSRKMLFVLAHTDQVSGLLRASFLLAQQRL	956
human	RGRWALRLCLEERDWLP GKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRL	958
rat	RGRRALRLCLEDRDWLP GQTLEFNLWASIYGSRKTLFVLAHTDKVSGLLRTSFLLAQQRL	958
	*** *****.**:*****.*.*** :*** :*.******:*****	
feline	LEDKRDVVVLVILRPDAHRSRYVRLRQRLCRQSVLLWPHQPSPGQRSFWAQLGALTALTRDNQ	1016
canine	LEDKRDVVVLVILCPDAHRSRYVRLRQRLCRQSVLLWPHQPSPGQRSFWAQLGALTALTRDNR	1018
bovine	LEDKRDVVVLVILRPAAYSRYVRLRQRLCRQSVLLWPHQPSPGQGSFWANLGIALTRDNR	1014
mouse	LEDKRDVVVLVILRPAAYSRYVRLRQRLCRQSVLLWPHQPSPGQGSFWANLGIALTRDNR	1014
ovine	LEDKRDVVVLVILRPAAYSRYVRLRQRLCRQSVLLWPHQPSPGQGSFWANLGIALTRDNR	1014
porcine	LEDKRDVVVLVILRPDAYRSRYVRLRQRLCRQSVLLWPHQPSPGQGSFWAQLGALTALTRDNH	1015
horse	LEDKRDVVVLVILSPDARRSYVRLRQRLCRQSVLFWPHQPSPGQRSFWAQLGALTALTRDNR	1016
human	LEDKRDVVVLVILSPDGRRSYVRLRQRLCRQSVLLWPHQPSPGQRSFWAQLGALTALTRDNH	1018
rat	LEDKRDVVVLVILRPDAHRSRYVRLRQRLCRQSVLFWPHQPNGQGSFWAQLGALTALTRDNH	1018
	*****.*.*****.*:***** ** ****.*.*****:	
feline	HFYQNFCRGPTTAE-----	1031
canine	HFYQNFCRGPTTA-----	1032
bovine	HFYNRNFCRGPTTAE-----	1029
mouse	HFYNRNFCRGPTTAE-----	1032
ovine	HFYNRNFCRGPTTAE-----	1029
porcine	HFYNRNFCRGPTTAE-----	1030
horse	HFYQNFCRGPTMAE-----	1031
human	HFYNRNFCQGPTAE-----	1032
rat	HFYNRNFCRGPTAE-----	1032
	*****.******	

Figure 2

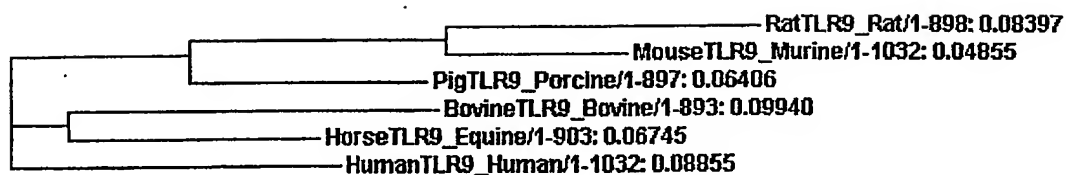
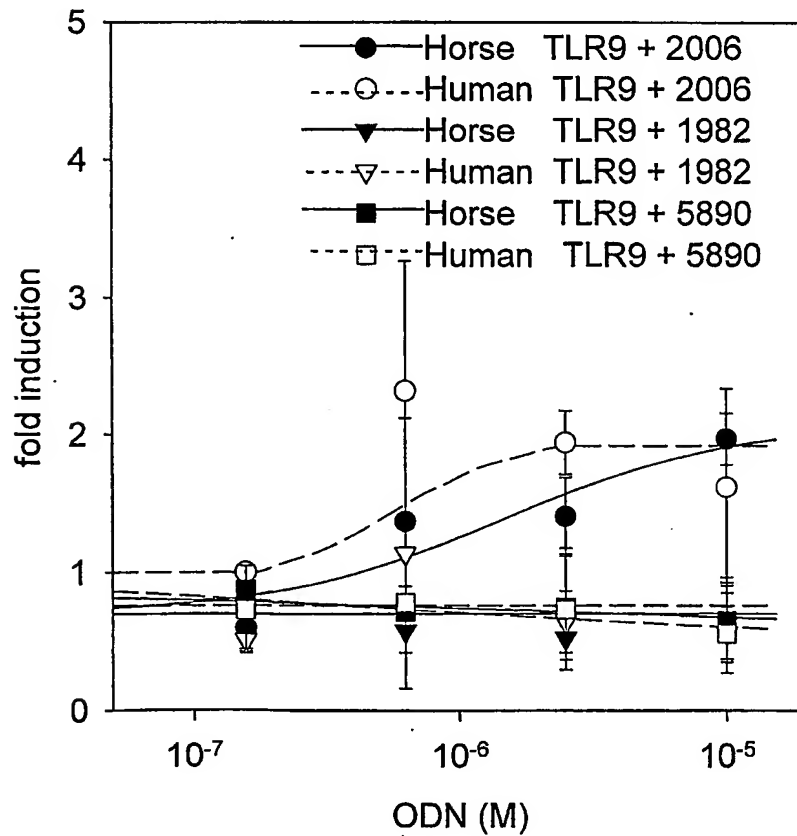


Figure 3



## SEQUENCE LISTING

<110> Coley Pharmaceutical GmbH  
University of Saskatchewan  
Qiagen GmbH

<120> TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

<130> C1041.70040WO00

<150> US 60/412,479

<151> 2002-09-19

<160> 70

<170> PatentIn version 3.1

<210> 1

<211> 1032

<212> PRT

<213> Rattus norvegicus

<400> 1

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn  
50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn  
65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met  
100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu  
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro  
 180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser  
 260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe  
 290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu  
 325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala  
 340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu  
 355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu  
 370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met  
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala  
405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr  
420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val  
435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser  
450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu  
465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala  
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp  
515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu  
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser  
565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val  
580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly  
595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe

610	615	620
Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys		
625	630	635 640
Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu		
	645	650 655
Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser		
	660	665 670
Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn		
	675	680 685
Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu		
	690	695 700
Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala		
705	710	715 720
Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn		
	725	730 735
Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn		
	740	745 750
Leu Thr Val Leu Asp Val Ser Ser Asn Pro Leu His Cys Ala Cys Gly		
	755	760 765
Ala Pro Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly		
	770	775 780
Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Arg Gln Leu Gln Gly Arg		
785	790	795 800
Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Asp Val Leu Ser		
	805	810 815
Arg Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Thr Val		
	820	825 830
Leu Pro Leu Leu Gln His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe		
	835	840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Thr Arg Gly Arg Arg Ser  
 850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
 865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu  
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp  
 900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr  
 915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Lys Val Ser  
 930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Phe Trp Pro His Gln Pro Asn Gly Gln Gly Ser Phe Trp Ala Gln  
 995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu  
 1025 1030

<210> 2  
 <211> 821  
 <212> PRT  
 <213> Rattus norvegicus

<400> 2

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15



Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn  
50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn  
65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met  
100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu  
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly  
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro  
180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu  
225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg  
245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser  
 260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe  
 290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu  
 325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala  
 340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu  
 355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu  
 370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala  
 405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr  
 420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val  
 435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser  
 450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu  
 465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
 485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala  
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp  
515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu  
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser  
565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val  
580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly  
595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe  
610 615 620

Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys  
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu  
645 650 655

Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser  
660 665 670

Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn  
675 680 685

Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala  
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn

725                      730                      735  
 Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn  
           740                      745                      750  
 Leu Thr Val Leu Asp Val Ser Ser Asn Pro Leu His Cys Ala Cys Gly  
           755                      760                      765  
 Ala Pro Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly  
           770                      775                      780  
 Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Arg Gln Leu Gln Gly Arg  
 785                      790                      795                      800  
 Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Asp Val Leu Ser  
           805                      810                      815  
 Arg Asp Cys Phe Gly  
           820

<210> 3  
 <211> 3099  
 <212> DNA  
 <213> Rattus norvegicus

<400> 3  
 atggttctct gtcgcaggac cctgcacccc ttgtctctcc tggtagaggc cgcagtgtctg 60  
 gctgaggctc tggccctggg taccctgcct gccttctctac cctgtgaact gaagcctcat 120  
 ggccctggtag actgcaactg gctcttctctg aagtctgtgc ctcacttctc tgccgcagaa 180  
 ccccgttcca acatcaccag cctttccttg atcgccaacc gcatccacca cctgcacaac 240  
 ctgacttttg tccacctgcc caacgtgcga cagctgaacc tcaagtggaa ctgtccgccc 300  
 cctggcctca gcccttgca cttctctctgc cgcattgacca ttgagcccaa aaccttctctg 360  
 gctatgcgca tgetggaaga gctgaacctg agctataacg gtatcaccac tgtgccccgc 420  
 ctgcccagct ccctgacgaa tctgagccta agccacacca acatcctggt actcgatgcc 480  
 agcagcctcg ctggcctgca cagcctgcga gttctcttca tggacgggaa ctgctactac 540  
 aagaaccctt gcaacggggc ggtgaacgtg acccgggacg ccttctctggg cttgagcaac 600  
 ctcaccact tgctccctta gtataacaac ctcacagagg tgccccgcca actgcccccc 660  
 agcctggagt acctcctgct gtccctataac ctcacgtgca agctgggggc cgaagaccta 720  
 gccaacctga cctcccttgc aatgcttgat gtgggtggga attgccgtcg ctgtgatcac 780

gcccccgacc tctgtacaga atgccggcag aagtcacctg atctgcaccc tcagactttc 840  
 catcacctga gccaccttga aggcctggtg ctgaaggaca gttctctcca ctgctgaac 900  
 tccaagtggg tccagggctt gccgaacctc tcgggtgctgg acctaacga gaactttctc 960  
 tacgagagca tcaacaaaac cagcgccttt cagaacctga cccgtctgcg caagctcgac 1020  
 ctgtccttca attactgcaa gaaggtatcg ttcgcccgc tccacctggc aagttccttc 1080  
 aagagcctgg tgctgctgca ggagctgaac atgaacggca tcttcttccg cttactcaac 1140  
 aagaacacgc tcaggtggct ggctgggtctg cccaagctcc acacgctgca cttcaaagt 1200  
 aatttcatca accaggcgca gctcagcgct tttagtacct tccgagccct tcgctttgtg 1260  
 gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc ccccgaaaag 1320  
 gcagacgagg cggagaaggg ggttccatgg cctgcaagtc tcaccccagc tctcccagc 1380  
 actcccgctc caaagaactt catggtcagg tgtaagaacc tcagattcac catggacctg 1440  
 tctcggaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccatctccag 1500  
 tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccc 1560  
 ctgaccaacc tgaagggtgt ggacctgtcc tataacaagc tggacctgta ccattcgaaa 1620  
 tcgttcagtg agtcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc 1680  
 agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac 1740  
 cttagcctgg cacacaatga cattcacagc cgcgtgtcct cagcctcta cagcacctca 1800  
 gtggagtatc tggacttcag cggcaacggt gtgggcccga tgtgggacga ggaggacctt 1860  
 tacctctatt tcttccaaga cctgagaagc ctgattcatc tggacctgtc tcagaataag 1920  
 ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt 1980  
 ttccgtgaca atcacctctc tttctttaac tggagcagtc tggccttctt gcccaatctg 2040  
 cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaat 2100  
 ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc 2160  
 ttctttgctc tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact 2220  
 gtggatcgct cctgggtttg gccattgtg atgaacctga cggttctaga cgtgagcagc 2280  
 aacctctgct attgtgcctg cgggtgcaccc tttgtagact tactgctgga agtcgagacc 2340  
 aaggtgcctg gcctggctaa cgggtgtgaag tgtggcagtc cccgccagct gcagggccgc 2400  
 agcatctttg cgcaagacct gcggtgtgct ctggatgacg tcctttctcg ggactgcttt 2460  
 ggcctttcac tcctggctgt ggcggtgggc acggtgttgc ctttactgca gcctctctgc 2520  
 ggctgggacg tctgggtactg tttccatctg tgccctggcat ggctaccttt gctgacctgt 2580

ggccggcgca gcgccaagc tctcccttat gatgccttcg tgggtgttca taaggcgag 2640  
 agcgcggttg ctgactgggt gtataacgag cttcgagtgc ggctagagga gcggcgcggt 2700  
 cgccgagccc tacgcttggt tctggaggac cgagattggc tgcctggcca gacactcttc 2760  
 gagaacctct gggcctccat ctatggcagc cgcaagactc tgtttgtgct ggcccacacg 2820  
 gacaaggcca gtggcctcct gcgcaccagc ttcctgctgg ctcagcagcg cctgctggag 2880  
 gaccgcaagg acgtgggtgt gttgggtgat ctgcgccctg atgccaccg ctcgcgtac 2940  
 gtgcgactgc gccagcgctt ctgccgccag agtgtgctct tctggcccca tcagcccaac 3000  
 gggcagggca gcttctgggc ccagctgagt acagccctga ctagggacaa ccaccacttc 3060  
 tataaccgga acttctgccg gggacctaca gcagaatag 3099

<210> 4

<211> 2463

<212> DNA

<213> Rattus norvegicus

<400> 4

atggttctct gtgcaggac cctgcacccc ttgtctctcc tggtagaggc cgcagtgtctg 60  
 gctgaggctc tggccctggg taccctgcct gccttcctac cctgtgaact gaagcctcat 120  
 ggcctggtag actgcaactg gctcttcctg aagtctgtgc ctcacttctc tgccgcagaa 180  
 ccccgttcca acatcaccag cctttccttg atcgccaacc gcatccacca cctgcacaac 240  
 ctgcactttg tccacctgcc caacgtgcga cagctgaacc tcaagtggaa ctgtccgccc 300  
 cctggcctca gcccttgca cttctcctgc cgcctgacca ttgagcccaa aaccttcctg 360  
 gctatgcgca tgctggaaga gctgaacctg agctataacg gtatcaccac tgtgccccgc 420  
 ctgcccagct ccctgacgaa tctgagccta agccacacca acatcctggt actcgatgcc 480  
 agcagcctcg ctggcctgca cagcctgcga gttctcttca tggacgggaa ctgctactac 540  
 aagaacccct gcaacggggc ggtgaacgtg acccggagc ccttcctggg cttgagcaac 600  
 ctcacccact tgtcccttaa gtataacaac ctcacagagg tgccccgcca actgcccccc 660  
 agcctggagt acctcctgct gtcctataac ctcctgtca agctgggggc cgaagaccta 720  
 gccaacctga cctcccttcg aatgcttgat gtgggtggga attgccgtcg ctgtgatcac 780  
 gccccgacc tctgtacaga atgccggcag aagtccttg atctgcaccc tcagactttc 840  
 catcacctga gccaccttga aggcctggtg ctgaaggaca gttctctcca ctgctgaac 900  
 tccaagtggg tccagggctc ggccaacctc togggtgctg acctaaagca gaactttctc 960  
 tacgagagca tcaacaaaac cagcgccttt cagaacctga cccgtctgcg caagctcgac 1020

```

ctgtccttca attactgcaa gaaggatcgc ttcgcccgc tccacctggc aagttccttc 1080
aagagcctgg tgcgctgca ggagctgaac atgaacggca tcttcttccg cttactcaac 1140
aagaacacgc tcaggtggct ggctggctctg cccaagctcc acacgctgca ccttcaaattg 1200
aatttcattca accaggcgca gctcagcgtc tttagtacct tccgagccct tcgctttgtg 1260
gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc ccccgaaaag 1320
gcagacgagg cggagaaggg ggttccatgg cctgcaagtc tcaccccagc tctcccagc 1380
actcccgctc caaagaactt catggtcagg tgtaagaacc tcagattcac catggacctg 1440
tctcggaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccatctccag 1500
tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccc 1560
ctgaccaacc tgaagggtgt ggacctgtcc tataacaagc tggacctgta ccattcgaaa 1620
tcgttcagtg agtcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc 1680
agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac 1740
cttagcctgg cacacaatga cattcacagc cgcgtgtcct cacgcctcta cagcacctca 1800
gtggagtatc tggacttcag cggcaacggt gtgggcccga tgtgggacga ggaggacctt 1860
tacctctatt tcttccaaga cctgagaagc ctgattcatc tggacctgtc tcagaataag 1920
ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt 1980
ttccgtgaca atcacctctc tttctttaac tggagcagtc tggccttcc tcccaatctg 2040
cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaatt 2100
ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc 2160
ttctttgctc tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact 2220
gtggatcgct cctggtttgg gccattgtg atgaacctga cggttctaga cgtgagcagc 2280
aaccctctgc attgtgcctg cgggtgcacc tttgtagact tactgctgga agtgcagacc 2340
aagggtgcctg gcctggctaa cgggtgtgaag tgtggcagtc cccgccagct gcagggccgc 2400
agcatctttg cgcaagacct gcggtgtgtc ctggatgacg tcctttctcg ggactgcttt 2460
ggc 2463

```

```

<210> 5
<211> 1030
<212> PRT
<213> Sus scrofa

<400> 5

```

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val  
 1 5 10 15

Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn  
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr  
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu  
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr  
 145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn  
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly  
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala  
 225 230 235 240



Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro  
 260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg  
 290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg  
 325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln  
 370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu  
 405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro  
 435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp  
 450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg  
 465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg  
 485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn  
 500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser  
 515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro  
 530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met  
 545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu  
 565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln  
 580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp  
 595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln  
 610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His  
 625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His  
 645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu  
 660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu  
 675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg  
 690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe

705	710	715	720
Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu	725	730	735
Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys	740	745	750
Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr	755	760	765
Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro	770	775	780
Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile	785	790	795
Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn	805	810	815
Cys Phe Gly Ile Ser Leu Leu Ala Met Ala Leu Gly Leu Val Val Pro	820	825	830
Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu	835	840	845
Cys Leu Ala Trp Leu Pro His Arg Gly Gln Arg Arg Gly Ala Asp Ala	850	855	860
Leu Phe Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val	865	870	875
Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg	885	890	895
Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro	900	905	910
Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg	915	920	925
Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu	930	935	940

Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys  
 945 950 955 960

Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala Tyr Arg Ser Arg  
 965 970 975

Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp  
 980 985 990

Pro His Gln Pro Arg Gly Gln Gly Ser Phe Trp Ala Gln Leu Gly Thr  
 995 1000 1005

Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg Asn Phe Cys  
 1010 1015 1020

Arg Gly Pro Thr Thr Ala Glu  
 1025 1030

<210> 6  
 <211> 819  
 <212> PRT  
 <213> Sus scrofa

<400> 6

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val  
 1 5 10 15

Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn  
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr  
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu  
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr  
 145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn  
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly  
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro  
 260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg  
 290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg  
 325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln  
 370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu  
 405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro  
 435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp  
 450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg  
 465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg  
 485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn  
 500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser  
 515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro  
 530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met  
 545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu  
 565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln  
 580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp  
 595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln  
 610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His  
 625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His  
 645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu  
 660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu  
 675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg  
 690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe  
 705 710 715 720

Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu  
 725 730 735

Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys  
 740 745 750

Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr  
 755 760 765

Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro  
 770 775 780

Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile  
 785 790 795 800

Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn  
 805 810 815

Cys Phe Gly

&lt;210&gt; 7

&lt;211&gt; 3352

&lt;212&gt; DNA

&lt;213&gt; Sus scrofa

&lt;400&gt; 7

```

gagcacgaac atccttcact gtagctgctg cccggtctgc cagccagacc ctttggagaa      60
gacccactc cctgtcatgg gccccgctg caccctgcac cccctttctc tcctggtgca      120
ggtgacagcg ctggctgcgg ctctggccca gggcaggctg cctgccttcc tgccctgtga      180
gctccagccc cacggcctgg tgaactgcaa ctggctcttc ctgaagtccg tgccccactt      240
ctcggcggca gcgccccggg ccaacgtcac cagcctctcc ttactctcca accgcatcca      300
ccacctgcac gactccgact tcgtccacct gtccagccta cgaactctca acctcaagtg      360
gaactgcccc cgggctggcc tcagccccat gcacttcccc tgccacatga ccatcgagcc      420
caacaccttc ctggccgtgc ccacctgga ggagctgaac ctgagctaca acagcatcac      480
gaccgtgcct gccctgcccg actccctcgt gtccctgtcg ctgagccgca ccaacatcct      540
ggtgctagac cccacccacc tcactggcct acatgccctg cgctacctgt acatggatgg      600
caactgctac tacaagaacc cctgccaggg ggcgctggag gtggtgccgg gtgccctcct      660
cggcctgggc aacctcacac atctctcact caagtacaac aatctcacgg aggtgccccg      720
cagcctgccc ccagcctgg agaccctgct gttgtcctac aaccacattg tcacctgac      780
gcctgaggac ctggccaatc tgactgccct gcgcgtgctt gatgtggggg ggaactgccg      840
ccgctgtgac catgcccgca accctgcag ggagtgcca aaggaccacc ccaagctgca      900
ctctgacacc ttcagccacc tgagccgcct cgaaggcctg gtgttgaaag acagttctct      960
ctacaacctg gacaccaggt ggttccgagg cctggacagg ctccaagtgc tggacctgag     1020
tgagaacttc ctctacgact gcatcaccaa gaccacggcc ttccagggcc tggcccgact     1080
gcgcagcctc aacctgtcct tcaattacca caagaagggtg tcctttgccc acctgcacct     1140
ggcaccctcc tttgggcacc tccggtccct gaaggagctg gacatgcatg gcatcttctt     1200
ccgctcgctc agtgagacca cgctccaacc tctgggtccaa ctgcctatgc tccagaccct     1260
gcgcctgcag atgaacttca ttaaccaggc ccagctcagc atctttgggg ccttcctctg     1320
cctgctgtac gtggacctat cggacaaccg catcagcggg gctgcaaggc cagtggccat     1380
tactagggag gtggatggta gggagagggg ctggctgcct tccaggaacc tcgctccacg     1440
tccactggac actctccgct cagaggactt catgccaaac tgcaaggcct tcagcttcac     1500

```



cttggacctg tctcggaaca acctggtgac aatccagtcg gagatgtttg ctgcctctc 1560  
 acgcctcgag tgccctgcgc tgagccacaa cagcatctcc caggcgggtca atggctctca 1620  
 gtttgtgccg ctgaccagcc tgcgggtgct ggacctgtcc cacaacaagc tggacctgta 1680  
 tcacggggcg tcgttcacgg agctgccgag cctggaagca ctggacctca gctacaatag 1740  
 ccagcccttt accatgcagg gtgtggggcca caacctcagc ttcgtggccc agctgcccg 1800  
 cctgcgctac ctacgcctgg cgcacaatga catccatagc cgagtgtccc agcagctctg 1860  
 tagcgctca ctgtgcgccc tggactttag cggcaacgat ctgagccgga tgtgggctga 1920  
 gggagacctc tatctccgct tcttccaagg cctaagaagc ctagtctggc tggacctgtc 1980  
 ccagaaccac ctgcacaccc tcttgccagc tgccctggac aacctccca aaagcctgaa 2040  
 gcatctgcat ctccgtgaca ataacctggc cttcttcaac tggagcagcc tgacctcct 2100  
 gcccaagctg gaaacctgg acttggtgg aaaccagctg aaggccctaa gcaatggcag 2160  
 cctgccatct ggcaaccagc tgcggaggct ggacctcagt ggcaacagca tcggctttgt 2220  
 gaacctggc tcttttgccc tggccaagca gttagaagag ctcaacctca gcgccaatgc 2280  
 cctcaagaca gtggagccct cctggtttg ctcgatggtg ggcaacctga aagtccaga 2340  
 cgtgagcgcc aacctctgc actgtgcctg tggggcgacc ttcgtgggct tctgtctgga 2400  
 ggtacaggct gccgtgcctg ggctgcccag ccgctcaag tgtggcagtc cggggcagct 2460  
 ccagggccat agcatctttg cgcaagacct gcgcctctgc ctggatgaga ccctctctg 2520  
 gaactgtttt ggcatctcgc tgcctggccat ggccctgggc ctggttctgc ccatgctgca 2580  
 ccacctctgc ggctgggacc tctggtactg cttccacctg tgccctggcct ggctgcccc 2640  
 ccgagggcag cggcggggag cagacgccct gttctatgat gccttcgtgg tctttgacaa 2700  
 agctcagagt gctgtggccg actgggtgta caacgagctg cgggtgcagc tggaggagcg 2760  
 ccgtggggcg cgcgcaactg gcctgtgcct ggaggagcga gactgggtac ctggcaagac 2820  
 gctcttcgag aacctgtggg cctcagtcta cagcagccgc aagacctgt ttgtgctggc 2880  
 ccacacggac cgtgtcagcg gcctcttgcg tgccagtctc ctgctggccc agcagcgct 2940  
 gctggaggac cgcaaggacg ttgtagtgct ggtgatcctg cgcgccgatg cctaccgctc 3000  
 ccgtacgtg cggctgcgcc agcgctctg ccgccagagt gtcctcctct ggccccacca 3060  
 gcccgtggg cagggcagct tctggggcca gctgggcaca gccctgacca gggacaacca 3120  
 ccacttctat aaccggaact tctgccgggg cccacgaca gccgaatagc actgagtgac 3180  
 agcccagttg cccagcccc cctggatttg cctctctgcc tggggtgccc caacctgctt 3240  
 tgctcagcca caccactgct ctgctccctg tccccaccc cccccccag cctggcatgt 3300

aacatgtgcc caataaatgc taccggaggg ccaagaaaaa aaaaaaaaaa aa 3352

<210> 8

<211> 2457

<212> DNA

<213> Sus scrofa

<400> 8

atgggcccc getgcaccct gcacccccctt tctctcctgg tgcaggtgac agcgctggct 60  
 ggggtctctgg ccagggcag gctgcctgcc ttctgccct gtgagctcca gccccacggc 120  
 ctggtgaact gcaactggct ctctctgaag tccgtgcccc acttctcggc ggcagcgccc 180  
 cgggccaacg tcaccagcct ctcttactc tccaaccgca tccaccacct gcacgactcc 240  
 gacttcgtcc acctgtccag cctacgaact ctcaacctca agtggaaactg cccgccggct 300  
 ggctcagcc catgcactt ccctgccac atgaccatcg agcccaacac ctctctggcc 360  
 gtgcccaccc tggaggagct gaacctgagc tacaacagca tcacgacctg gcctgccctg 420  
 cccgactccc tegtgtccct gtgctgagc cgcaccaaca tcctgggtgt agacccccacc 480  
 cacctcactg gcctacatgc cctgcgtac ctgtacatgg atggcaactg ctactacaag 540  
 aaccctgcc agggggcgct ggaggtggtg ccgggtgccc tcctcggcct gggcaacctc 600  
 acacatctct cactcaagta caacaatctc acggaggtgc cccgcagcct gccccccagc 660  
 ctggagaccc tgctgttgtc ctacaaccac attgtcacc tgacgcctga ggacctggcc 720  
 aatctgactg ccctgcgcgt gcttgatgtg ggggggaact gccgccgtg tgacctgcc 780  
 cgcaaccct gcagggagtg cccaaaggac caccocaagc tgactctga caccttcagc 840  
 cacctgagcc gcctcgaagg cctggtgttg aaagacagtt ctctctacaa cctggacacc 900  
 aggtggttcc gaggcctgga caggctccaa gtgctggacc tgagtgagaa ctctctctac 960  
 gactgcatca ccaagaccac ggccttcag ggcctggccc gactgcgcag cctcaacctg 1020  
 tccttcaatt accacaagaa ggtgtccttt gccacctgc acctggcacc ctctttggg 1080  
 cacctccgtt cctgaagga gctggacatg catggcatct tcttcgctc gctcagttag 1140  
 accacgtcc aacctctggt ccaactgcct atgctccaga ccctgcgcct gcagatgaac 1200  
 ttcattaacc aggccagct cagcatcttt ggggccttcc ctggcctgct gtacgtggac 1260  
 ctatcggaca accgcatcag cggagctgca aggcagtggt ccattactag ggaggtggat 1320  
 ggtagggaga gggctctggct gccttcagg aacctcgctc cagctccact ggacactctc 1380  
 cgctcagagg acttcatgcc aaactgcaag gccttcagct tcaccttga cctgtctcgg 1440  
 aacaacctgg tgacaatcca gtcggagatg tttgctcgcc tctcacgcct cgagtgcctg 1500

cgctgagcc acaacagcat ctcccaggcg gtcaatggct ctcagtttgt gccgctgacc 1560  
 agcctgcggg tgctggacct gtcccacaac aagctggacc tgtatcacgg gcgctcgttc 1620  
 acggagctgc cgcgccctgga agcactggac ctcagctaca atagccagcc ctttaccatg 1680  
 caggggtgtgg gccacaacct cagcttcgtg gccagctgc ccgccctgcg ctacctcagc 1740  
 ctggcgcaca atgacatcca tagccgagtg tcccagcagc tctgtagcgc ctcactgtgc 1800  
 gccctggact ttagcggcaa cgatctgagc cggatgtggg ctgagggaga cctctatctc 1860  
 cgcttcttcc aaggcctaag aagcctagtc tggtctggacc tgtcccagaa ccacctgcac 1920  
 accctcctgc cagtgccct ggacaacctc cccaaaagcc tgaagcatct gcatctccgt 1980  
 gacaataacc tggccttctt caactggagc agcctgacct tcctgcccac gctggaaacc 2040  
 ctggacttgg ctggaaacca gctgaaggcc ctaagcaatg gcagcctgcc atctggcacc 2100  
 cagctgcgga ggctggacct cagtggcaac agcatcggtt ttgtgaaccc tggcttcttt 2160  
 gccctggcca agcagttaga agagctcaac ctcagcgcca atgccctcaa gacagtggag 2220  
 ccctcctggt ttggctcgat ggtgggcaac ctgaaagtcc tagacgtgag cgccaaccct 2280  
 ctgcactgtg cctgtggggc gaccttcgtg ggcttctctg tggaggtaca ggctgccgtg 2340  
 cctgggctgc ccagccgct caagtgtggc agtccggggc agctccaggg ccatagcatc 2400  
 tttgcgaag acctgcgcct ctgcctggat gagaccctct cgtggaactg ttttggc 2457

<210> 9

<211> 1029

<212> PRT

<213> Bos taurus

<400> 9

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr  
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly  
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala  
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr

305	310	315	320
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg	325	330	335
Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His	340	345	350
Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu	355	360	365
Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln	370	375	380
Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn	385	390	395
Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu	405	410	415
Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro	420	425	430
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu	435	440	445
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp	450	455	460
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn	465	470	475
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu	485	490	495
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly	500	505	510
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His	515	520	525
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln	530	535	540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln  
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg  
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys  
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu  
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly  
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr  
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu  
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val  
 705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly Leu Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met  
 820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys  
 835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu  
 850 855 860

Leu Tyr Asp Ala Val Val Val Phe Asp Lys Val Gln Ser Ala Val Ala  
 865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly  
 885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly  
 900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys  
 915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg  
 930 935 940

Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp  
 945 950 955 960

Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr  
 965 970 975

Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro  
 980 985 990

His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Ile Ala  
 995 1000 1005

Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg  
 1010 1015 1020

Gly Pro Thr Thr Ala Glu  
1025

<210> 10  
<211> 818  
<212> PRT  
<213> Bos taurus

<400> 10

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu  
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe  
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr  
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly  
180 185 190



Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
 260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
 290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg  
 325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln  
 370 375 380

Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro

420	425	430
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu		
435	440	445
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp		
450	455	460
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn		
465	470	475 480
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu		
485	490	495
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly		
500	505	510
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His		
515	520	525
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln		
530	535	540
Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln		
545	550	555 560
Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg		
565	570	575
Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys		
580	585	590
Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu		
595	600	605
Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly		
610	615	620
Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr		
625	630	635 640
Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu		
645	650	655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu  
690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val  
705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile  
740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg  
770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
805 810 815

Phe Gly

<210> 11

<211> 3191

<212> DNA

<213> Bos taurus

<400> 11

gggaagtggg cgccaagcat ccttcctgc agctgcctcc caacctgccc gccagaccct 60

ctggagaagc cgcattccct gtcattgggccc cctactgtgc cccgcacccc ctttctctcc 120

tgggtgcaggc ggcggcactg gcagcggccc tggccgaggg caccctgcct gccttctctgc 180

cctgtgagct ccagcccat ggtcagggtg actgcaactg gctgttctctg aagtctgtgc 240

cgcacttttc ggctggagcc ccccgggcca atgtcaccag cctctcctta atctccaacc 300

gcatccacca cttgcatgac tctgacttgc tccacctgtc caacctgcgg gtcctcaacc 360  
 tcaagtggaa ctgcccgcg gccggcctca gcccctgca cttcccctgc cgtatgacca 420  
 tcgagcccaa caccttcctg gctgtgcca ccctggagga gctgaacctg agctacaacg 480  
 gcatcacgac cgtgectgcc ctgcccagtt cctcgtgtc cctgtcgtg agccacacca 540  
 gcatcctggt gctaggcccc accacttca ccggcctgca cgccctgcgc tttctgtaca 600  
 tggacggcaa ctgctactac atgaacctt gccgcgggc cctggaggtg gccccaggcg 660  
 ccctcctcgg cctgggcaac ctcacgcacc tgtcgtcaa gtacaacaac ctcacggagg 720  
 tgccccgcg cctgcccccc agcctggaca ccctgctgt gtcctacaac cacattgtca 780  
 ccctggcacc cgaggacctg gccaacctga ctgccctgcg cgtgcttgac gtgggtggga 840  
 actgccgcg ctgcgacctat gcccgcaacc cctgcaggga gtgcccagg aacttcccca 900  
 agctgcaccc tgacaccttc agtcacctga gccgcctcga aggcctggtg ttgaaggaca 960  
 gttctctcta caaactagag aaagattggt tccgcggcct gggcaggctc caagtgtcgt 1020  
 acctgagtga gaacttcctc tatgactaca tcaccaagac caccatcttc aacgacctga 1080  
 cccagctgcg cagactcaac ctgtccttca attaccaca gaaggtgtcc ttcgcccacc 1140  
 tgcaacctagc gtcctccttt gggagtctgg tgtccctgga gaagctggac atgcacggca 1200  
 tcttcttcg ctcctcacc aacatcacgc tccagtcgt gaccgcgtg cccaagctcc 1260  
 agagtctgca tctgcagctg aacttcatca accaggccca gctcagcatc tttggggcct 1320  
 tcccagacct gctcttcgtg gacctgtcgg acaaccgcat cagcggagcc gcgacgccag 1380  
 cggccgcctt gggggagggtg gacagcaggg tggaagtctg gcgattgcc aggggcctcg 1440  
 ctccaggccc gctggacgcc gtcagctcaa aggacttcat gccaagctgc aacctcaact 1500  
 tcaccttga cctgtcacgg aacaacctgg tgacaatcca gcaagagatg tttaccgcgc 1560  
 tctccgcct ccagtgcctg cgcctgagcc acaacagcat ctgcaggcg gttaatggct 1620  
 cccagttcgt gccgtgacc agcctgcgag tgctcgacct gtcccacaac aagctggacc 1680  
 tgtaccatgg gcgctcattc acggagctgc cgcagctgga ggcaactggac ctcagctaca 1740  
 acagccagcc cttcagcatg cagggcgtgg gccacaacct cagcttcgtg gccagctgc 1800  
 cctccctgcg ctacctcagc cttgcgcaca atggcatcca cagccgcgtg tcacagaagc 1860  
 tcagcagcgc ctcttgcgc gccctggact tcagcggcaa ctccctgagc cagatgtggg 1920  
 ccgagggaga cctctatctc tgctttttca aaggcttgag gaacctggtc cagctggacc 1980  
 tgtccgagaa ccctctgcac accctcctgc ctgcctacct ggacaacctg cccaagagcc 2040

tgcggcagct gcgtctccgg gacaataacc tggccttctt caactggagc agcctgaccg 2100  
 tcctgccccg gctggaagcc ctggatctgg caggaaacca gctgaaggcc ctgagcaacg 2160  
 gcagcctgcc gcctggcatc cggctccaga agctggacgt gagcagcaac agcatcggct 2220  
 tcgtgatecc cggtttcttc gtccgcgga ctcggctgat ~~agcgttaac~~ ctcagcgcca 2280  
 atgccctgaa ~~gacagtggat~~ ccttcctggg tgggttcctt agcagggacc ctgaaaatcc 2340  
 tagacgtgag cgccaaccgc ctccactgcg cctgcggggc ggcctttgtg gacttcctgc 2400  
 tggagagaca ggaggccgtg cccgggctgt ccaggcgcgt cacatgtggc agtccggggc 2460  
 agtccaggg ccgcagcatc ttcacacagg acctgcgcct ctgcctggat gagaccctct 2520  
 ccttggaactg ctttggcctc tcaactgctaa tgggtggcgt gggcctggca gtgcccattg 2580  
 tgcaccacct ctgtggtgg gacctctgg actgcttcca cctgtgtctg gccatttgc 2640  
 cccgacggcg gcggcagcgg ggcgaggaca cctgctcta tgatgccgtc gtggtcttcg 2700  
 acaagggtgca gagtgcagtg gctgattggg tgtacaacga gctccgcgtg cagctggagg 2760  
 agcgcggggg gcgccggcg ctcgcctct gcctggagga gcgagactgg ctccctggta 2820  
 agacgtctct cgagaacctg tgggcctcgg tctacagcag ccgcaagacc atgttcgtgc 2880  
 tggaccacac ggaccgggtc agcggcctcc tgcgcgccag ctctctgctg gccagcagc 2940  
 gcctgttgga ggaccgcaag gacgtcgtag tgctggtgat cctgcgccc gccgcctatc 3000  
 ggtcccgcta cgtgcggctg cgcagcgcc tctgcgcga gagcgtctc ctctggcccc 3060  
 accagcccag tggccagggt agtttctggg ccaacctgg catagccctg accagggaca 3120  
 accgtcactt ctataaccgg aacttctgcc ggggccccac gacagccgaa tagcacagag 3180  
 tgactgccc a g 3191

<210> 12  
 <211> 2454  
 <212> DNA  
 <213> Bos taurus

<400> 12  
 atgggcccct actgtgcccc gaacccctt tctctcctgg tgcaggcggc ggcaactggca 60  
 gcggccctgg ccgagggcac cctgcctgcc ttctgcct gtgagctcca gccccatggt 120  
 cagggtggact gcaactggct gttcctgaag tctgtgcgc acttttcggc tggagcccc 180  
 cgggccaatg tcaccagcct ctcttaata tccaaccgca tccaccactt gcatgactct 240  
 gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtggaaactg cccgcgggc 300  
 ggcctcagcc ccatgcactt cccctgcctg atgaccatcg agcccaacac ctctctgggt 360

gtgcccaccc tggaggagct gaacctgagc tacaacggca tcacgaccgt gcctgccctg 420  
 cccagttccc tcgtgtccct gtcgctgagc cacaccagca tcctggtgct agggcccacc 480  
 cacttcaccg gcctgcacgc cctgcgcttt ctgtacatgg acggcaactg ctactacatg 540  
 aacccctgcc cgcgggccct ggaggtggcc ccaggcgccc tcctcggcct gggcaacctc 600  
 acgcacctgt cgctcaagta caacaacctc acggaggtgc ccgcccgcct gcccaccagc 660  
 ctggacaccc tgctgctgtc ctacaaccac attgtcaccc tggcaccga ggacctggcc 720  
 aacctgactg ccctgcgcgt gcttgacgtg ggtgggaact gccgcgcgtg cgaccatgcc 780  
 cgcaaccctt gcagggagtgc ccaaagaac ttccccaagc tgcaccctga caccttcagt 840  
 cacctgagcc gcctcgaagg cctggtgttg aaggacagtt ctctctacaa actagagaaa 900  
 gattggttcc gcggcctggg caggctccaa gtgctcgacc tgagtgagaa cttcctctat 960  
 gactacatca ccaagaccac catcttcaac gacctgacc agctgcgcag actcaacctg 1020  
 tccttcaatt accacaagaa ggtgtccttc gccacactgc acctagcgtc ctcctttggg 1080  
 agtctggtgt ccctggagaa gctggacatg cacggcatct tcttcgcctc cctcaccaac 1140  
 atcacgctcc agtcgctgac ccggctgccc aagctccaga gtctgcatct gcagctgaac 1200  
 ttcacaaacc agggccagct cagcatcttt ggggccttcc cgagcctgct cttcgtggac 1260  
 ctgtcggaca accgcatcag cggagccgag acgccagcgg ccgcccctggg ggaggtggac 1320  
 agcaggggtg aagtctggcg attgcccagg ggcctcgctc caggcccgtt ggacgcccgtc 1380  
 agctcaaagg acttcatgcc aagctgcaac ctcaacttca ccttgacact gtcacggaac 1440  
 aacctggtga caatccagca agagatgttt accgcctct cccgcctcca gtgcctgcgc 1500  
 ctgagccaca acagcatctc gcaggcggtt aatggctccc agttcgtgcc gctgaccagc 1560  
 ctgcgagtgc tcgacctgtc ccacaacaag ctggacctgt accatgggag ctcattcacg 1620  
 gagctgccgc agctggaggc actggacctc agctacaaca gccagccctt cagcatgcag 1680  
 ggcgtggggc acaacctcag cttcgtggcc cagctgccct ccctgcgcta cctcagcctt 1740  
 gcgcacaatg gcatccacag ccgctgttca cagaagctca gcagcgctc gttgcgcgcc 1800  
 ctggacttca gcggcaactc cctgagccag atgtgggccc agggagacct ctatctctgc 1860  
 tttttcaaag gcttgaggaa cctggtccag ctggacctgt ccgagaacca tctgcacacc 1920  
 ctctgcctc gtcacctgga caacctgccc aagagcctgc ggcagctgcg tctccgggac 1980  
 aataacctgg ccttcttcaa ctggagcagc ctgacctcc tgcgccggt ggaagccctg 2040  
 gatctggcag gaaaccagct gaaggccctg agcaacggca gcctgccgcc tggcatccgg 2100  
 ctccagaagc tggacgtgag cagcaacagc atcggtctcg tgatccccgg cttcttcgtc 2160

cgcgcgactc ggctgataga gcttaacctc agcgccaatg ccctgaagac agtggatccc 2220  
 tcctgggttcg gttccttagc agggaccctg aaaatcctag acgtgagcgc caaccgctc 2280  
 cactgcgcct gcggggcggc ctttgtggac ttcctgctgg agagacagga ggccgtgccc 2340  
 gggctgtcca ggcgcgctac atgtggcagt ccgggccagc tccagggccg cagcatcttc 2400  
 acacaggacc tgcgccctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 13  
 <211> 1031  
 <212> PRT  
 <213> Equus caballus

<400> 13

Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met  
 100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
 130 135 140

Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro  
 145 150 155 160

Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe  
 260 265 270

Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe  
 290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu  
 370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met  
 385 390 395 400



Asn	Phe	Ile	Asn	Gln	Ala	Gln	Leu	Gly	Ile	Phe	Lys	Asp	Phe	Pro	Gly	
				405					410						415	
Leu	Arg	Tyr	Ile	Asp	Leu	Ser	Asp	Asn	Arg	Ile	Ser	Gly	Ala	Val	Glu	
			420					425					430			
Pro	Val	Ala	Thr	Thr	Gly	Glu	Val	Asp	Gly	Gly	Lys	Lys	Val	Trp	Leu	
		435					440					445				
Thr	Ser	Arg	Asp	Leu	Thr	Pro	Gly	Pro	Leu	Asp	Thr	Pro	Ser	Ser	Glu	
	450					455					460					
Asp	Phe	Met	Pro	Ser	Cys	Lys	Asn	Leu	Ser	Phe	Thr	Leu	Asp	Leu	Ser	
465					470					475					480	
Arg	Asn	Asn	Leu	Val	Thr	Val	Gln	Pro	Glu	Met	Phe	Ala	Gln	Leu	Ser	
				485					490						495	
Arg	Leu	Gln	Cys	Leu	Arg	Leu	Ser	His	Asn	Ser	Ile	Ser	Gln	Ala	Val	
			500					505					510			
Asn	Gly	Ser	Gln	Phe	Val	Pro	Leu	Thr	Ser	Leu	Gln	Val	Leu	Asp	Leu	
		515					520					525				
Ser	His	Asn	Lys	Leu	Asp	Leu	Tyr	His	Gly	Arg	Ser	Phe	Thr	Glu	Leu	
	530					535					540					
Pro	Arg	Leu	Glu	Ala	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	Gln	Pro	Phe	Ser	
545					550					555					560	
Met	Arg	Gly	Val	Gly	His	Asn	Leu	Ser	Phe	Val	Ala	Gln	Leu	Pro	Thr	
				565					570						575	
Leu	Arg	Tyr	Leu	Ser	Leu	Ala	His	Asn	Gly	Ile	His	Ser	Arg	Val	Ser	
			580					585					590			
Gln	Gln	Leu	Cys	Ser	Thr	Ser	Leu	Trp	Ala	Leu	Asp	Phe	Ser	Gly	Asn	
		595					600					605				
Ser	Leu	Ser	Gln	Met	Trp	Ala	Glu	Gly	Asp	Leu	Tyr	Leu	Arg	Phe	Phe	
	610					615					620					
Gln	Gly	Leu	Arg	Ser	Leu	Ile	Arg	Leu	Asp	Leu	Ser	Gln	Asn	Arg	Leu	
625					630					635					640	

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln  
 645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
 660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln  
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln  
 690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe  
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
 725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu  
 740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
 755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu  
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser  
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp  
 805 810 815

Asp Cys Phe Gly Leu Ser Leu Leu Val Val Ala Leu Gly Leu Ala Met  
 820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His  
 835 840 845

Leu Gly Leu Ala Trp Leu Pro Arg Arg Gly Trp Gln Arg Gly Ala Asp  
 850 855 860

Ala Leu Ser Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala

865                      870                      875                      880  
 Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg  
                                  885                      890                      895  
 Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu  
                                  900                      905                      910  
 Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser  
                                  915                      920                      925  
 Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Gln Val Ser Gly Leu  
                                  930                      935                      940  
 Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg  
                                  945                      950                      955                      960  
 Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Ala Arg Arg Ser  
                                  965                      970                      975  
 Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Phe  
                                  980                      985                      990  
 Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly  
                                  995                      1000                      1005  
 Met Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln Asn Phe  
                                  1010                      1015                      1020  
 Cys Arg Gly Pro Thr Met Ala Glu  
                                  1025                      1030  
  
 <210> 14  
 <211> 820  
 <212> PRT  
 <213> Equus caballus  
  
 <400> 14  
  
 Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln  
 1                      5                      10                      15  
  
 Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe  
                                  20                      25                      30  
  
 Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu

35	40	45
Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn		
50	55	60
Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp		
65	70	75
Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp		
85	90	95
Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met		
100	105	110
Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu		
115	120	125
Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser		
130	135	140
Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro		
145	150	155
Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly		
165	170	175
Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro		
180	185	190
Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr		
195	200	205
Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr		
210	215	220
Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu		
225	230	235
Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg		
245	250	255
Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe		
260	265	270

Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe  
 290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu  
 370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly  
 405 410 415

Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu  
 420 425 430

Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu  
 435 440 445

Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu  
 450 455 460

Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser  
 465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser  
 485 490 495

Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val  
 500 505 510

Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560

Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr  
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser  
 580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn  
 595 600 605

Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe  
 610 615 620

Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu  
 625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln  
 645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
 660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln  
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln  
 690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe  
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
 725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu  
 740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
 755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu  
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser  
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp  
 805 810 815

Asp Cys Phe Gly  
 820

<210> 15  
 <211> 3391  
 <212> DNA  
 <213> Equus caballus

<400> 15  
 ctctgtttctc tgagctgttg ccgcgtgaag ggactgcgag cacaaagcat cctcctctgc 60  
 agctgctgcc cagtgtgcc gctggacct ctggatcatc tccactccc tgtcatgggc 120  
 ccttgccatg gtgccctgca gccctgtct ctctgtgtgc aggcggccat gctggccgtg 180  
 gctctggccc aaggcacct gcctcccttc ctgccctgtg agctccagcc ccacggcctg 240  
 gtgaactgca actggctgtt cctgaagtcc gtgccccact tctcagcagc agcaccgccg 300  
 gacaatgtca ccagccttcc cttgtctctc aaccgcatcc accacctcca cgactccgac 360  
 tttgcccac tgtccaacct gcagaaactc aacctcaaat ggaactgccc gccagccggc 420  
 ctcagcccca tgcacttccc ctgccacatg accatcgagc ccaacacttt cctggctgta 480  
 cccaccctgg aggagctgaa cctgagctac aacggcatca cgactgtgcc tgccctgccc 540  
 agctccctcg tgtccctgat cctgagccgc accaaccatc tgcagctaga cccaccagc 600  
 ctcacggggc tgcattgccct gcgcttccta tacatggatg gcaactgcta ctacaagaac 660  
 ccctgcgggc gggccctgga ggtggcccca ggcgcctcc ttggcctggg caacctcacc 720  
 cacctgtcac tcaagtacaa caacctcaca acggtgcccc gcagcctgcc ccctagcctg 780  
 gagtacctgc tgttgtccta caaccacatt gtcaccctgg cacctgagga cctggccaat 840  
 ctgactgccc tgcgtgtgct cgatgtgggt ggaaactgcc gccgctgtga ccatgcacgc 900  
 aaccctgctg tggagtgccc acataaatcc cccagctgc actccgacac cttcagccac 960

ctaagccgcc tagaaggcct cgtgttgaag gatagttctc tctaccagct gaaccccaga 1020  
 tggttccgtg gcctgggcaa cctcacagtg ctccagctga gtgagaactt cctctacgac 1080  
 tgcattacca aaaccaaggc attccagggc ctggcccagc tgcgaagact caacttgtcc 1140  
 ttcaattacc ataagaaggc gtccttcgcc cacctgacgc tggcaccctc cttcggggagc 1200  
 ctgctctccc tgcaggaact ggacatgcat ggcatcttct tccgctcact cagccagaag 1260  
 acgctccagc cactggcccc cctgcccatg ctccagcgtc tgtatctgca gatgaacttc 1320  
 atcaaccagg ccagctcgg catcttcaag gacttccctg gtctgcgcta catagacctg 1380  
 tcagacaacc gcatcagtgg agctgtggag ccggtggcca ccacagggga ggtggatggt 1440  
 gggaagaagg tctggctgac atccagggac ctactccag gccactgga cccccagc 1500  
 tctgaggact tcattgccaag ctgcaagaac ctgagcttca ccttggaact gtcacggaac 1560  
 aacctggtaa cagtccagcc agagatgttt gccagctct cgcgcctcca gtgcctgcgc 1620  
 ctgagccaca acagcatctc gcaggcggtc aatggctcac agttcgtgcc actgaccagc 1680  
 ctgcagggtg tggacctgtc ccataacaaa ctggacctgt accatgggag ctcgtttacg 1740  
 gagctgccgc gactggaggc cctggacctc agctacaaca gccagccctt cagcatgcgg 1800  
 ggtgtggggc acaacctcag ctttgtggcc cagctgcca ccctgcgcta cctcagcctg 1860  
 gcacacaatg gcatccacag ccgtgtgtcc cagcagctct gcagcacctc gctgtggggc 1920  
 ctggacttca ggggcaattc cctgagccag atgtgggctg agggagacct ctatctccgc 1980  
 ttcttccaag gcctgagaag cctaaccgg ctagacctgt ccagaatcg tctgcatacc 2040  
 ctctgccat gcacctggg caacctcccc aagagcttgc agctgctgcg tctccgtaac 2100  
 aattacctgg ccttcttcaa ttggagcagc ctgacctcc tgcaccaact ggaaacctg 2160  
 gacctggctg gaaaccagct gaaggctctg agcaatggca gcctgccttc tggcaccag 2220  
 ctccagaggc tggacgtcag caggaacagc atcatcttcg tggccctggt cttctttgct 2280  
 ctggccacga ggctgcgaga gctcaacctc agtgccaacg ccctcaggac agaggagccc 2340  
 tcctggtttg gtttcttagc aggtccctt gaagtcttag atgtgagcgc caacctctg 2400  
 cactgcgcct gtggggcagc ctttgtggac ttctgctgc aggttcaggc tgccgtgcct 2460  
 ggtctgcca gccgcgtcaa gtgtggcagt ccgggcccag tccagggccg cagcatcttc 2520  
 gcacaagacc tgcgcctctg cctggacaag tccctctcct gggactgttt tggctctctca 2580  
 ttgctggttg tggccctggg cctggccatg cctatgttgc accacctctg cggctgggac 2640  
 ctctggtaact gcttccacct gggcctggcc tggctgcccc ggccgggggtg gcagcggggc 2700



gcggatgccc tgagctatga tgcctttgtg gtcttcgaca aggcacagag cgcagtggcc 2760  
 gactgggtgt acaatgaact gcgggtgccc ctagaggagc gccgtgggag cggggcgctc 2820  
 cgctgtgtc tggaggagcg tgactggcta cctggcaaga cgctgttcga aaacctgtgg 2880  
 gcctcagtct acagcagccg caagatgctg tttgtgctgg cccacacgga ccaggtcagt 2940  
 ggctctctgc gtgccagctt cctgctggcc cagcagcgtc tgctggagga ccgcaaggac 3000  
 gttgtggtgc tggtaatcct gagccctgac gcccgcggtt cccgttacgt ggggctgctc 3060  
 cagcgcctct gccgccagag tgcctcttc tggtcccacc agcctagtgg ccagcgcagc 3120  
 ttctggggcc agctaggcat ggccctgacc agggacaacc gccacttcta taaccagaac 3180  
 ttctgccggg gcccgacgat ggctgagtag cacagagtga cagcctggca tgtacaacc 3240  
 ccagccctga ccttgctct ctgcctatga tgccagctc gcctcactct gtgacgcccc 3300  
 tgctctgct ccgccacct caccctggc atacagcagg cactcaataa atgccactgg 3360  
 caggccaaac agccaaaaa aaaaaaaaaa a 3391

<210> 16  
 <211> 2460  
 <212> DNA  
 <213> Equus caballus

<400> 16  
 atggggcctt gccatggtgc cctgcagccc ctgtctctcc tgggtgcaggc ggccatgctg 60  
 gccgtggctc tggcccaagg caccctgcct ccttctctgc cctgtgagct ccagcccccac 120  
 ggctggtga actgcaactg gctgttctct aagtccgtgc cccacttctc agcagcagca 180  
 ccccgaggaca atgtcaccag cctttctctg ctctccaacc gcatccacca cctccacgac 240  
 tccgactttg cccaactgtc caacctgcag aaactcaacc tcaaattgaa ctgcccgcga 300  
 gccggcctca gcccctatgca cttcccctgc cacatgacca tcgagcccaa cactttctctg 360  
 gctgtaccca cctggagga gctgaacctg agctacaacg gcatcacgac tgtgcctgcc 420  
 ctgcccagct cctcgtgtc cctgatcctg agccgcacca acatcctgca gctagacccc 480  
 accagcctca cgggcctgca tgccctgctc ttcctataca tggatggcaa ctgctactac 540  
 aagaaccctt gcggggcggc cctggaggtg gcccagggc ccctccttgg cctgggcaac 600  
 ctcaccacc tgctactcaa gtacaacaac ctcacaacgg tgccccgcag cctgccccct 660  
 agcctggagt acctgctgtt gtctacaac cacattgtca ccctggcacc tgaggacctg 720  
 gccaatctga ctgccctgcg tgtgctcgat gtgggtggaa actgccgccg ctgtgaccat 780  
 gcaagcaacc cctgcgtgga gtgccacat aaattcccc agctgcactc cgacaccttc 840

agccacctaa gccgcctaga aggcctcgtg ttgaaggata gttctctcta ccagctgaac 900  
 cccagatggg tccgtggcct gggcaacctc acagtgcctg acctgagtga gaacttcctc 960  
 tacgactgca tcacaaaaac caaggcatte cagggcctgg cccagctgcg aagactcaac 1020  
 ttgtccttca attaccataa gaagggtgctc ttcgcccacc tgacgctggc accctccttc 1080  
 gggagcctgc tctccctgca ggaactggac atgcatggca tcttcttccg ctcaactcagc 1140  
 cagaagacgc tccagccact ggcccgctg cccatgctcc agcgtctgta tctgcagatg 1200  
 aacttcatca accaggccca gctcggcatc ttcaaggact tccctgggtct gcgctacata 1260  
 gacctgtcag acaaccgcat cagtggagct gtggagccgg tggccaccac aggggaggtg 1320  
 gatgggtggga agaagggtctg gctgacatcc agggacctca ctccaggccc actggacacc 1380  
 cccagctctg aggacttcat gccaaagtgc aagaacctca gcttcacctt ggacctgtca 1440  
 cggaacaacc tggtaacagt ccagccagag atgtttgccc agctctcgcg cctccagtgc 1500  
 ctgcgcctga gccacaacag catctcgcag gcggtcaatg gctcacagtt cgtgccactg 1560  
 accagcctgc aggtgctgga cctgtcccat aacaaactgg acctgtacca tgggcgctcg 1620  
 ttacggagc tgccgcgact ggaggccctg gacctcagct acaacagcca gcccttcagc 1680  
 atgcggggtg tgggccacaa cctcagcttt gtggcccagc tgcccaccct gcgctacctc 1740  
 agcctggcac acaatggcat ccacagccgt gtgtcccagc agctctgcag cacctcgtg 1800  
 tgggccctgg acttcagcgg caattccctg agccagatgt gggctgaggg agacctctat 1860  
 ctccgcttct tccaaggcct gagaagccta atccggctag acctgtccca gaatcgtctg 1920  
 cataccctcc tgccatgcac cctgggcaac ctcccaga gcttgcagct gctgcgtctc 1980  
 cgtaacaatt acctggcctt cttcaattgg agcagcctga ccctcctgcc caacctggaa 2040  
 acctggacc tggctggaaa ccagctgaag gctctgagca atggcagcct gccttctggc 2100  
 accagctcc agaggctgga cgtcagcagg aacagcatca tcttcgtggg ccctggcttc 2160  
 tttgctctgg ccacgaggct gcgagagctc aacctcagt ccaacgccct caggacagag 2220  
 gagccctcct ggtttggttt cctagcaggc tcccttgaag tcctagatgt gagcgccaac 2280  
 cctctgcact gcgcctgtgg ggcagccttt gtggacttcc tgctgcaggt tcaggctgcc 2340  
 gtgcctggtc tgcccagccg cgtcaagtgt ggcagtccgg gccagctcca gggccgcagc 2400  
 atcttcgcac aagacctgcg cctctgcctg gacaagtccc tctcctggga ctgttttggg 2460

&lt;210&gt; 17

&lt;211&gt; 1029

&lt;212&gt; PRT

&lt;213&gt; Ovis aries

&lt;400&gt; 17

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr  
 145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly  
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
 260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
 290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg  
 325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg  
 370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp  
 435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp  
 450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn  
 465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu  
 485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly  
 500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr  
 515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln  
 530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln  
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg  
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys  
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu  
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly  
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr  
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu  
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val  
 705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly Phe Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met  
 820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys  
 835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu  
 850 855 860

Leu Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val Ala  
 865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly  
 885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly  
 900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys  
 915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg

930                      935                      940  
 Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp  
 945                      950                      955                      960  
 Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr  
                     965                      970                      975  
 Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro  
                     980                      985                      990  
 His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Met Ala  
                     995                      1000                      1005  
 Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg  
                     1010                      1015                      1020  
 Gly Pro Thr Thr Ala Glu  
                     1025  
  
 <210> 18  
 <211> 818  
 <212> PRT  
 <213> Ovis aries  
  
 <400> 18  
 Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1                      5                      10                      15  
  
 Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu  
                     20                      25                      30  
  
 Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe  
                     35                      40                      45  
  
 Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
                     50                      55                      60  
  
 Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65                      70                      75                      80  
  
 Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
                     85                      90                      95  
  
 Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr

100	105	110
Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn		
115	120	125
Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu		
130	135	140
Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr		
145	150	155
His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn		
165	170	175
Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly		
180	185	190
Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn		
195	200	205
Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu		
210	215	220
Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala		
225	230	235
Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg		
245	250	255
Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro		
260	265	270
Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu		
275	280	285
Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg		
290	295	300
Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr		
305	310	315
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg		
325	330	335



Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg  
 370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp  
 435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp  
 450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn  
 465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu  
 485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly  
 500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr  
 515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln  
 530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln  
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg  
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys  
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu  
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly  
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr  
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu  
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val  
 705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly

&lt;210&gt; 19

&lt;211&gt; 3199

&lt;212&gt; DNA

<213> *Ovis aries*

&lt;400&gt; 19

```

gtcggcacgg gaagtgagcg ccaagcatcc ttccctgcag ctgccgcca acttgcccgc      60
cagaccctct ggagaagccg cattccctgc catgggcccc tactgtgccc cgcaccccct      120
ttctctcttg gtgcaggcgg cggcgctggc agcagccctg gccagggca ccctgcctgc      180
cttcctgccc tgtgagctcc agccccgggg taagggtgaac tgcaactggc tgttcctgaa      240
gtctgtgccc cgcttttcgg cgggagcccc cggggccaat gtcaccagcc tctccttaat      300
ctccaaccgc atccaccact tgcacgactc tgacttcgtc cacctgtcca acctgcccgt      360
cctcaacctc aagtggaact gcccgccggc cggcctcagc cccatgcact tcccctgccc      420
catgaccatc gagcccaaca ccttcctggc tgtgcccacc ctggaggagc tgaacctgag      480
ctacaatggc atcacgaccg tgccctgcct gccagttct ctcgatccc tgcgctgag      540
ccgaccagc atcctggtgc taggccccac ccacttcacc ggctgcacg ccctgcgctt      600
tctgtacatg gacggcaact gctactataa gaaccctgc cagcaggccg tggaggtggc      660
cccaggcgcc ctccctggcc tgggcaacct cacgcacctg tcgctcaagt acaacaacct      720
cacggaggtg ccccgccgcc tgccccccag cctggacacc ctgctgctgt cctacaacca      780
catcatcacc ctggcaccgg aggacctggc caatctgact gccctgcgtg tgcttgatgt      840
ggcggggaac tgccgcgct gcgaccacgc ccgaacccc tgcagggagt gcccaaagaa      900
cttccccaag ctgcacctg acaccttcag ccacctgagc cgcctcgaag gcctggtgtt      960
gaaggacagt tctctctaca aactagagaa agactggttc cgcggcctgg gcaggctcca     1020
agtgtctgac ctgagtgaga acttctctta tgactacatc accaagacca ccattctcag     1080
gaacctgacc cagctgcgca gactcaacct gtccttcaat taccacaaga aggtgtcctt     1140
cgccacctg caactggcac cctcctttgg gggcctggtg tccctggaga agctggacat     1200
gcacggcatc ttcttccgct ccctcaccaa caccacgctc cggccgctga ccagctgcc     1260
caagctccag agtctgagtc tgcagctgaa cttcatcaac caggccgagc tcagatctt     1320
tggggccttc ccgagcctgc tcttcgtgga cctgtcggac aaccgcatca gcggagctgc     1380
gaggccggtg gccgccctcg gggaggtgga cagcggggtg gaagtctggc ggtggcccag     1440

```

gggcctcgct ccaggcccgc tggccgcccgt cagcgcaaaag gacttcatgc caagctgcaa 1500  
 cctcaacttc accttggacc tgtcacggaa caacctggtg acgatccagc aggagatgtt 1560  
 taccgccttc tcccgcctcc agtgectgcg cctgagccac aacagcatct cgcaggcggt 1620  
 taatggctcg cagttcgtgc cgctgacctg cctgcgagtg ctcgacctgt cctacaacaa 1680  
 gctggacctg taccatgggc gctcgttcac ggagctgccg cagctggagg cactggacct 1740  
 cagctacaac agccagccct tcagcatgca gggcgtgggc cacaacctca gcttcgtggc 1800  
 ccagctgccg tccctgcgct acctcagcct tgcgcacaaac ggcatccaca gccgcgtgtc 1860  
 acagaagctc agcagcgctt cgctgcgcgc cctggacttc agcggcaact ccctgagcca 1920  
 gatgtggggc gagggagacc tctatctctg cttcttcaaa ggcttgagga acctggtcca 1980  
 gctggacctg tccaagaacc acctgcacac cctcctgcct cgtcacctgg ataacctgcc 2040  
 caagagcctg cggcagctgc gtctccggga caataacctg gccttcttca actggagcag 2100  
 cctgactgtt ctgccccagc tggaagccct ggatctggcg ggaaaccagc tgaaggccct 2160  
 gagcaacggc agcctgccac ctggcaccgc gctccagaag ctggacgtga gcagcaacag 2220  
 catcggttt gtgacctctg gcttctttgt ccttgccaac cggtgaaag agcttaacct 2280  
 cagcgccaac gccctgaaga cagtggatcc cttctggttc ggtcgcttaa cagagacct 2340  
 gaatattcta gacgtgagcg ccaaccgcct ccactgtgcc tgcggggcgg cctttgtgga 2400  
 cttcctgctg gagatgcagg cgcccggtcc tgggctgtcc aggcgcgtca cgtgtggcag 2460  
 tccggggcag ctccagggcc gcagcatctt cgcacaggac ctgcgcctct gcctggatga 2520  
 gacctctctc ttggactgct ttggcttctc gctgctaata gtggcgctgg gcctggcggt 2580  
 gcccatgctg caccacctct gtggctggga cctgtggtac tgcttccacc tgtgtctggc 2640  
 ccatttgccc cgacggcggc ggcagcgggg cgaggacacc ctgctctacg atgccttctg 2700  
 ggtcttcgac aaggcgcaga gtgcagtggc cgactgggtg tacaacgagc tccgcgtgca 2760  
 gctggaggag cgccgcgggc gccgggcgct ccgcctctgc ctggaggagc gagactggct 2820  
 ccctggcaag acgctcttcg agaacctgtg ggcctcggtc tacagcagcc gtaagaccat 2880  
 gttcgtgctg gaccacacgg accgggtcag tggcctcctg cgcgccagct tcctgtggc 2940  
 ccagcagcgc ctgttgagg accgcaagga tgtcgtggtg ctggtgatcc tgcgccccgc 3000  
 cgcctaccgg tcccgtacg tgcggctgcg ccagcgctc tgccgccaga gcgtcctct 3060  
 ctggcccccac cagcccagtg gccaggtag cttctggggc aacctgggca tggccctgac 3120  
 cagggacaac cgccacttct ataaccggaa cttctgcgcg ggcgccga cagccgaata 3180

gcacagagtg actgcccag

3199

&lt;210&gt; 20

&lt;211&gt; 2454

&lt;212&gt; DNA

<213> *Ovis aries*

&lt;400&gt; 20

atggggccct actgtgcccc gcacccctt tctctcctgg tgcaggcggc ggcgctggca	60
gcagccctgg cccagggcac cctgcctgcc ttcttgccct gtgagctcca gcccgggggt	120
aaggtgaact gcaactggct gttcctgaag tctgtgccgc gcttttcggc cggagccccc	180
cgggccaatg tcaccagcct ctccttaatc tccaaccgca tccaccactt gcacgactct	240
gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtggaactg cccgccggcc	300
ggcctcagcc ccattgcactt cccctgccgc atgaccatcg agcccaacac cttcctggct	360
gtgcccaccc tggaggagct gaacctgagc tacaatggca tcacgaccgt gcctgacctg	420
cccagttctc tcgtatccct gtgcctgagc cgcaccagca tcctggtgct agggcccacc	480
cacttcaccg gcctgcacgc cctgcgcttt ctgtacatgg acggcaactg ctactataag	540
aaccctgcc agcaggccgt ggaggtggcc ccaggcgccc tccttggcct gggcaacctc	600
acgcacctgt cgctcaagta caacaacctc acggagggtgc cccgcgcctt gccccccagc	660
ctggacaccc tgctgctgtc ctacaaccac atcatcacc tggcaccoga ggacctggcc	720
aatctgactg ccctgcgtgt gcttgatgtg ggcgggaact gccgccgctg cgaccacgcc	780
cgcaaccctt gcagggagtg cccaaagaac ttccccaaagc tgcacctga caccttcagc	840
cacctgagcc gcctcgaagg cctgggtgtg aaggacagtt ctctctacaa actagagaaa	900
gactggttcc gcggcctggg caggctccaa gtgctcgacc tgagtgagaa cttcctctat	960
gactacatca ccaagaccac catcttcagg aacctgacct agctgcgcag actcaacctg	1020
tccttcaatt accacaagaa ggtgtccttc gccacctgc aactggcacc ctcctttggg	1080
ggcctgggtg ccctggagaa gctggacatg cacggcatct tcttcgctc cctcaccaac	1140
accacgtccc ggccgctgac ccagctgccc aagctccaga gtctgagtct gcagctgaac	1200
ttcatcaacc aggcagagct cagcatcttt ggggccttcc cgagcctgct cttcgtggac	1260
ctgtcggaca accgcatcag cggagctgcg aggcgggtgg ccgccctcgg ggaggtggac	1320
agcgggggtg aagtctggcg gtggcccagg ggcctcgctc caggcccgtt ggccgcccgtc	1380
agcgcaaagg acttcatgcc aagctgcaac ctcaacttca ccttggacct gtcacggaac	1440
aacctggtga cgatccagca ggagatgttt acccgccctc cccgcctcca gtgcctgcgc	1500

ctgagccaca acagcatctc gcaggcggtt aatggctcgc agttcgtgcc gctgaccgcg 1560  
 ctgcgagtgc tcgacctgtc ctacaacaag ctggacctgt accatgggcg ctcggttcacg 1620  
 gagctgccgc agctggaggc actggacctc agctacaaca gccagccctt cagcatgcag 1680  
 ggcgtggggc acaacctcag cttcgtggcc cagctgccgt cctgcgcta cctcagcctt 1740  
 gcgcacaacg gcatccacag ccgcgtgtca cagaagctca gcagcgctc gctgcgcgcc 1800  
 ctggacttca gcggcaactc cctgagccag atgtggggcg agggagacct ctatctctgc 1860  
 ttcttcaaag gcttgaggaa cctgggtccag ctggacctgt ccaagaacca cctgcacacc 1920  
 ctctgcctc gtcacctgga taacctgcc aagagcctgc ggcagctgcg tctccgggac 1980  
 aataacctgg ccttcttcaa ctggagcagc ctgactgttc tgcccagct ggaagccctg 2040  
 gatctggcgg gaaaccagct gaaggccctg agcaacggca gcctgccacc tggcaccgcg 2100  
 ctccagaagc tggacgtgag cagcaacagc atcggctttg tgaccctgg cttctttgtc 2160  
 cttgccaacc ggctgaaaga gcttaacctc agcgccaacg ccctgaagac agtggatccc 2220  
 ttctggttcg gtcgcttaac agagaccctg aatatactag acgtgagcgc caaccgctc 2280  
 cactgtgcct gcggggcgcc ctttgtggac ttctgtctgg agatgcaggc ggccgtgcct 2340  
 gggctgtcca ggcggtcac gtgtggcagt ccgggccagc tccagggccg cagcatcttc 2400  
 gcacaggacc tgcgcctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 21

<211> 1032

<212> PRT

<213> Canis familiaris

<400> 21

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn  
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
65 70 75 80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu  
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly  
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro  
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
195 200 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe  
260 265 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly  
275 280 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe  
290 295 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu  
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu  
370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu  
385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu  
420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val  
435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly  
450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp  
465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg  
485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln  
500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu  
515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr  
530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro



545	550	555	560
Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu	565	570	575
Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg	580	585	590
Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser	595	600	605
Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg	610	615	620
Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn	625	630	635
Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser	645	650	655
Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp	660	665	670
Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly	675	680	685
Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln	690	695	700
Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro	705	710	715
Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala	725	730	735
Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly	740	745	750
Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys	755	760	765
Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro	770	775	780

Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly  
 785 790 795 800

Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu  
 805 810 815

Ser Trp Val Cys Phe Ser Leu Ser Leu Leu Ala Val Ala Leu Ser Leu  
 820 825 830

Ala Val Pro Met Leu His Gln Leu Cys Gly Trp Asp Leu Trp Tyr Cys  
 835 840 845

Phe His Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly  
 850 855 860

Val Asp Ala Leu Ala Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
 865 870 875 880

Ser Ser Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu  
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp  
 900 905 910

Trp Val Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr  
 915 920 925

Ser Ser Arg Lys Thr Leu Phe Val Leu Ala Arg Thr Asp Arg Val Ser  
 930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Cys Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln  
 995 1000 1005

Leu Gly Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Thr Ala  
1025 1030

<210> 22  
<211> 822  
<212> PRT  
<213> Canis familiaris

<400> 22

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn  
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
65 70 75 80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu  
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly  
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro  
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe  
 260 265 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe  
 290 295 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu  
 370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu  
 385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu  
 420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val  
 435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly  
 450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp  
 465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg  
 485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln  
 500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu  
 515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr  
 530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro  
 545 550 555 560

Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu  
 565 570 575

Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg  
 580 585 590

Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser  
 595 600 605

Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg  
 610 615 620

Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn  
 625 630 635 640

Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser  
 645 650 655

Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp

660                                      665                                      670  
 Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly  
       675                                      680                                      685  
 Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln  
       690                                      695                                      700  
 Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro  
       705                                      710                                      715                                      720  
 Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala  
                                     725                                      730                                      735  
 Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly  
                                     740                                      745                                      750  
 Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys  
                                     755                                      760                                      765  
 Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro  
       770                                      775                                      780  
 Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly  
       785                                      790                                      795                                      800  
 Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu  
                                     805                                      810                                      815  
 Ser Trp Val Cys Phe Ser  
                                     820

<210> 23  
 <211> 3334  
 <212> DNA  
 <213> Canis familiaris

<400> 23  
 aggaaggggc tgtgagctcc aagcatcctt tctgcagct gctgcccagc ctgccagcca 60  
 gaccctctgg agaagcccc gctccctgtc atgggccctt gccgtggcgc cctgcacccc 120  
 ctgtctctcc tgggtgcaggc tgccgcgcta gccctggccc tggcccaggg caccctgcct 180  
 gccttctgc cctgtgagct ccagcccat ggctgtgga actgcaactg gctgttcctc 240  
 aagtccgtgc cccgcttctc ggcagctgca cccgcggta acgtcaccag cctttccttg 300

tactccaacc gcatccacca cctccatgac tatgactttg tccacttcgt ccacctgcgg	360
cgtctcaatc tcaagtggaa ctgcccgcgc gccagcctca gcccctgca ctttccctgt	420
cacatgacca ttgagcccaa caccttcctg gctgtgcca ccctagagga cctgaatctg	480
agctataaca gcatcacgac tgtgcccgc ctgccagtt cgcttggtc cctgtccctg	540
agccgcacca acatcctggt gctggaccct gccaccctgg caggccttta tgccctgcgc	600
ttcctgttcc tggatggcaa ctgctactac aagaaccct gccagcaggc cctgcaggtg	660
gcccaggtg ccctcctggg cctgggcaac ctcacacacc tgtcactcaa gtacaacaac	720
ctcaccgtgg tgccgcgggg cctgcccccc agcctggagt acctgctctt gtccataaac	780
cacatcatca ccctggcacc tgaggacctg gccaatctga ctgccctgcg tgcctcgat	840
gtgggtggga actgtcgccg ctgtgaccat gccgtaacc cctgcaggga gtgcccgaag	900
ggcttcccc agctgcaccc caacaccttc ggccacctga gccacctga aggcctggtg	960
ttgagggaca gctctctcta cagcctggac ccaggtggt tccatggcct gggcaacctc	1020
atggtgctgg acctgagtga gaacttcctg tatgactgca tcacaaaac caaagccttc	1080
tacggcctgg ccggtctgcg cagactcaac ctgtccttca attatcataa gaagggtgcc	1140
tttgeccacc tgcctctggc atcctccttc gggagcctac tgtccctgca ggagctggac	1200
atacatggca tcttcttccg ctgctcagc aagaccacgc tccagtcgct ggcccacctg	1260
cccatgctcc agcgtctgca tctgcagttg aactttatca gccaggccca gctcagcatc	1320
ttcggcgctt tccttgact gcggtacgtg gacttgctag acaaccgcat cagtggagct	1380
gcagagcccc cggtgccac aggggaggta gaggcagact gtggggagag agtctggcca	1440
cagtccccgg accttgctct gggcccactg ggcacccccg gctcagaggc cttcatgccg	1500
agctgcagga ccctcaactt caccttgga ctgtctcgga acaacctagt gactgttcag	1560
ccggagatgt ttgtccggt ggcgcgcctc cagtgcctgg gcctgagcca caacagcatc	1620
tcgcaggcgg tcaatggctc gcagttcgtg cctctgagca acctgcgggt gctggacctg	1680
tcccataaca agctggacct gtaccacggg cgctcgttca cggagctgcc gcggtggag	1740
gccttggaac tcagctacaa cagccagccc ttcagcatgc ggggcgtggg ccacaatctc	1800
agctttgtgg cacagctgcc agcctgcgc tacctcagcc tggcgcacaa tggcatccac	1860
agccgcgtgt ccagcagct ccgcagcgcc tcgctccggg ccctggactt cagtggcaat	1920
acctgagcc agatgtgggc cgaggagac ctctatctcc gcttcttcca aggcctgaga	1980
agcctggttc agctggacct gtcccagaat cgctgcata ccctcctgcc acgcaacctg	2040
gacaacctcc ccaagagcct ggggtcctg cggtccgtg acaattacct ggctttcttc	2100

```

aactggagca gcctggccct cctacccaag ctggaagccc tggacctggc gggaaaccag 2160
ctgaaggccc tgagcaatgg cagcttgccc aacggcacc cagctccagag gctggacctc 2220
agcggcaaca gcacggcctt cgtgggtccc agcttttttg ccctggccgt gaggcttcga 2280
gagctcaacc tcagcgccaa cgcctcaag acggtggagc cctcctgggt tggttccctg 2340
gcgggtgccc tgaaagtctt agacgtgacc gccaaccctt tgcatcgcc ttgcggcgca 2400
accttcgtgg acttcttgct ggaggtgcag gctgcgggtg ccggcctgcc tagccgtgtc 2460
aagtgcggca gcccgggcca gctccagggc cgcagcatct tcgcacagga cctgcgcctc 2520
tgcttgagc aagcgtcttc ctgggtctgt ttcagcctct cgtgctggc tgtggccctg 2580
agcctggctg tgcccatgct gcaccagctc tgtggctggg acctctggta ctgcttcac 2640
ctgtgcctgg cctggctgcc ccggcggggg cggcgggggg gtgtggatgc cctggcctat 2700
gacgccttcg tggctctcga caaggcgcag agctcgggtg cggactgggt gtacaatgag 2760
ctgcgggtac agctagagga gcgcgtggg cgcggggcgc tacgcctgtg tctggaggaa 2820
cgtgactggg taccggcaa aacctcttc gagaacctct gggcctcagt ttacagcagc 2880
cgcaagacgc tgtttgtgct ggcccgacg gacagagtca gcggcctcct gcgtgccagc 2940
ttcctgctgg cccaacagcg cctgctggag gaccgcaagg acgtcgtggg gctgggtgac 3000
ctgtgccccg acgcccaccg ctcccgtat gtgcggctgc gccagcgcct ctgccgccag 3060
agtgtcctcc tctggcccca ccagcccagt ggccagcgca gcttctgggc ccagctgggc 3120
acggccctga ccagggacaa ccgccacttc tacaaccaga acttctgccg gggccccacg 3180
acagcctgat aggcagacag cccagcacct tcgcgccctt acacctgcc tgtctgtctg 3240
ggatgcccga cctgctggct ctacaccgcc gctctgtctc cctacaccc agccctggca 3300
taaagcgacc gctcaataaa tgctgctggg agac 3334

```

&lt;210&gt; 24

&lt;211&gt; 2466

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;400&gt; 24

```

atgggcccc ggcgtgggc cctgcacccc ctgtctctcc tggcgcaggc tgccgcgcta 60
gccttgcccc tggcccaggg caccctgcct gccttcctgc cctgtgagct ccagcccat 120
ggcctgggtga actgcaactg gctgttcctc aagtccgtgc cccgcttctc ggcagctgca 180
ccccgcggta acgtcaccag cctttccttg tactccaacc gcacccacca cctccatgac 240
tatgactttg tccacttcgt ccacctgcgg cgtctcaatc tcaagtggaa ctgcccgcgc 300

```



gccagcctca gcccacatgca ctttcctctgt cacatgacca ttgagcccaa caccttcctg 360  
gctgtgcccc ccctagagga cctgaatctg agctataaca gcatcacgac tgtgcccgcc 420  
ctgcccagtt cgcttgtgtc cctgtccctg agccgcacca acatcctggt gctggaccct 480  
gccaccctgg caggccttta tgcctgctg cctctgttcc tggatggcaa ctgctactac 540  
aagaaccctt gccagcaggc cctgcaggtg gcccaggtg ccctcctggg cctgggcaac 600  
ctcacacacc tgtcactcaa gtacaacaac ctccacgtgg tgcgcgggg cctgcccccc 660  
agcctggagt acctgtctt gtctacaac cacatcatca ccctggcacc tgaggacctg 720  
gccaatctga ctgcccctgcg tgcctcgat gtgggtggga actgtcgccg ctgtgaccat 780  
gcccgttaacc cctgcaggga gtgcccgaag ggcttcccc agctgcacc caacaccttc 840  
ggccacctga gccacctga aggcctggtg ttgagggaca gctctctcta cagcctggac 900  
cccaggtggt tccatggcct gggcaacctc atggtgctgg acctgagtga gaacttcctg 960  
tatgactgca tcacaaaaac caaagccttc tacggcctgg cccggctgcg cagactcaac 1020  
ctgtccttca attatcataa gaaggtgtcc tttgccacc tgcactggc atcctccttc 1080  
gggagcctac tgtccctgca ggagctggac atacatggca tcttcttccg ctgctcagc 1140  
aagaccacgc tccagtcgct ggccacctg cccatgtctc agcgtctgca tctgcagttg 1200  
aactttatca gccaggccca gctcagcatc ttcgggcct tccctggact gcggtacgtg 1260  
gacttgtcag acaaccgcat cagtggagct gcagagccc cggctgccac aggggaggta 1320  
gaggcagact gtggggagag agtctggcca cagtccggg accttgcctt gggccactg 1380  
ggcaccctcg gctcagaggc ctctatgccg agctgcagga ccctcaactt caccttggac 1440  
ctgtctcgga acaacctagt gactgttcag ccggagatgt ttgtccggct ggcgcgctc 1500  
cagtgcctgg gcctgagcca caacagcatc tgcaggcgg tcaatggctc gcagtctgtg 1560  
cctctgagca acctgcgggt gctggacctg tcccataaca agctggacct gtaccacggg 1620  
cgctcgttca cggagctgcc gcggctggag gccttggacc tcagctacaa cagccagccc 1680  
ttcagcatgc ggggcgtggg ccacaatctc agctttgtgg cacagctgcc agccctgcgc 1740  
tacctcagcc tggcgacaaa tggcatccac agccgcgtgt cccagcagct ccgcagcgcc 1800  
tcgctccggg ccctggactt cagtggcaat accctgagcc agatgtgggc cgaggagac 1860  
ctctatctcc gcttcttcca aggcctgaga agcctggctt agctggacct gtcccagaat 1920  
cgctgcata ccctcctgcc acgcaacctg gacaacctcc ccaagagcct gcggctcctg 1980  
cggctccgtg acaattacct ggctttcttc aactggagca gcctggcctt cctacccaag 2040

ctggaagccc tggacctggc gggaaaccag ctgaaggccc tgagcaatgg cagcttgccc 2100  
 aacggcaccc agctccagag gctggacctc agcggcaaca gcatcggctt cgtgggtcccc 2160  
 agcttttttg ccctggccgt gaggttcga gagtcaacc tcagcgccaa cgccctcaag 2220  
 acggtggagc cctcctgggt tggttccctg gcgggtgccc tgaaagtcct agacgtgacc 2280  
 gccaacccct tgcattgcgc ttgcggcgca accttcgtgg acttcttgct ggaggtgcag 2340  
 gctgcgggtgc cgggcctgcc tagccgtgtc aagtgcggca gcccgggcca gctccagggc 2400  
 cgcagcatct tcgcacagga cctgcgcctc tgcttgagc aagcgctctc ctgggtctgt 2460  
 ttcagc 2466

<210> 25  
 <211> 1031  
 <212> PRT  
 <213> Felis catus

<400> 25

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
 100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
 130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
 145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe  
 260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe  
 290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu  
 370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu  
 420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu  
 435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu  
 450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser  
 465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser  
 485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val  
 500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala  
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser  
 580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
 595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe

610	615	620
Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu		
625	630	635 640
His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg		
	645	650 655
Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser		
	660	665 670
Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln		
	675	680 685
Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln		
	690	695 700
Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe		
	705	710 715 720
Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala		
	725	730 735
Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu		
	740	745 750
Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala		
	755	760 765
Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu		
	770	775 780
Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser		
	785	790 795 800
Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp		
	805	810 815
Asp Cys Phe Gly Leu Ser Leu Leu Thr Val Ala Leu Gly Leu Ala Val		
	820	825 830
Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His		
	835	840 845

Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly Ala Asp  
 850 855 860

Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala  
 865 870 875 880

Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg  
 885 890 895

Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu  
 900 905 910

Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser  
 915 920 925

Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu  
 930 935 940

Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg  
 945 950 955 960

Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His Arg Ser  
 965 970 975

Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu  
 980 985 990

Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly  
 995 1000 1005

Thr Ala Leu Thr Arg Asp Asn Gln His Phe Tyr Asn Gln Asn Phe  
 1010 1015 1020

Cys Arg Gly Pro Thr Thr Ala Glu  
 1025 1030

<210> 26

<211> 820

<212> PRT

<213> Felis catus

<400> 26

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn  
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly  
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro  
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe  
 260 265 270

~~Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly~~  
~~275 280 285~~

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe  
 290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu  
 370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu  
 420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu  
 435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu  
 450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser  
 465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser  
 485 490 495



Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val  
500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala  
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser  
580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe  
610 615 620

Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu  
625 630 635 640

His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg  
645 650 655

Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
660 665 670

Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln  
675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln  
690 695 700

Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe  
705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala

725	730	735
Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu 740 745 750		
Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala 755 760 765		
Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu 770 775 780		
Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser 785 790 795 800		
Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp 805 810 815		
Asp Cys Phe Gly 820		

```
<210> 27
<211> 3235
<212> DNA
<213> Felis catus
```

<400>	27
agggtctgcg agctccaggc attcttctct gccatcgctg cccagtctgc catccagacc	60
ctctggagaa gccccactc cctgtcatgg gcccctgcc tggcgccctg cccccctgt	120
ctctcctggg gcaggctgcc gcgctggccg tgGCCctggc ccagggcacc ctgcctgcct	180
ttctgCCctg tgagctccag cgccacggcc tGGtgAattg cgactggctg ttctcaagt	240
cGtgCCCCa cttctcgGcg gcagcgcccc gtggtAACgt caccagcctt tcctgtact	300
ccaaccgcat ccaccacct caCgactccg actttgtCCA cctgtccagc ctgCGgcgtc	360
tCAacctcaa atggaactgc CCaccGCCa gcctcagccc catgcacttc cCctgtcaca	420
Tgaccattga gccccacacc ttcttgGccg tgcccaccct ggaggagctg aaCctgagct	480
acaacagcat cacgacagta cccgCCctgc ccagttccct cgtgtccctg tccttgagcc	540
GtacCaacat cctggTgctg gaccctGCCa acctcgCagg gctgcactcc ctgcgctttc	600
Tgttcttgga tggcaactgc tactacaaga acccctgccc gcaggccctg caggtggccc	660
cggcgccct ccttgGcctg ggcaacctta cgcacctgtc actcaagtac aacaacctca	720
ctgcggtgcc ccgCGgcctg cccccagcc tggagtacct gctattgtcc tacaaccaca	780

tcataccacct	ggcacctgag	gacctggcca	acctgaccgc	cctgcgtgtg	ctcgatgtgg	840
gtgggaactg	ccgtcgctgt	gaccacgccc	gcaaccctg	tatggagtgc	cccaagggt	900
tcccgcacct	gcacctgac	accttcagcc	acctgaacca	cctcgaaggc	ctgggtgtga	960
aggacagctc	tctctacaac	ctgaaccca	gatgggtcca	tgcctgggc	aacctcatgg	1020
tgctggacct	gagtgagaac	ttcctatatg	actgcatcac	caaaaccaca	gccttccagg	1080
gcctggcca	gctgcgcaga	ctcaacttgt	ctttcaatta	ccacaagaag	gtgtccttgg	1140
cccacctgca	tctggcgccc	tccttcggga	gcctgctctc	cctgcagcag	ctggacatgc	1200
atggcatctt	cttcgcctcg	ctcagcgaga	ccacgctccg	gtcgtgtgtc	cacctgcca	1260
tgctccagag	tctgcacctg	cagatgaact	tcataatca	ggcccagctc	agcatcttcg	1320
gggccttccc	tggcctgcca	tacgtggacc	tgtagacaa	ccgcataagt	ggagccatgg	1380
agctggcggc	tgccacgggg	gaggtggatg	gtggggagag	agtcgggtg	ccatctgggg	1440
acctagctct	gggcccaccg	ggcacccta	gctccgagg	cttcatgcca	ggctgcaaga	1500
ccctcaactt	caccttggac	ctgtcacgga	acaacctagt	gacaatccag	ccagagatgt	1560
ttgcccggct	ctcgccctc	cagtgcctgc	tcctgagccg	caacagcatc	tcgaggcag	1620
tcaacggctc	acaatttatg	ccgctgacca	gcctgcagg	gctggacctg	tcccataaca	1680
agctggacct	gtaccatggg	cgctctttca	cggagctgcc	gcggctggag	gccctggacc	1740
tcagctacaa	cagccagccc	ttcagcatgc	agggcgtggg	tcacaacctc	agctttgtgg	1800
cacagctgcc	ggccctgcgc	tatctcagcc	tgccgcacaa	cgacatccac	agccgtgtgt	1860
cccagcagct	ctgcagcgcc	tcgctgcggg	ccttggactt	cagcggcaat	gccttgagcc	1920
ggatgtgggc	cgaggagac	ctgtatctcc	acttcttccg	aggcctgagg	agcctggtcc	1980
ggttggatct	gtcccagaat	cgctgcata	ccctcttgcc	acgcacctg	gacaacctcc	2040
ccaagagcct	gcggctgctg	cgtctccgtg	acaattatct	ggctttcttc	aactggagca	2100
gcctggtcct	cctccccagg	ctggaagccc	tggacctggc	gggaaaccag	ctgaaggccc	2160
tgagcaacgg	cagcttgctc	aatggaaccc	agctccagag	gctggacctc	agcagcaaca	2220
gtatcagctt	cgtggcctcc	agcttttttg	ctctggccac	caggctgcga	gagctcaacc	2280
tcagtgcmaa	cgccctcaag	acggtggagc	cctcctgggt	cggttctcta	gcgggcaccc	2340
tgaaagtcct	agatgtgact	ggcaaccccc	tgactgcgc	ctgtggggcg	gccttcgtgg	2400
acttcttgct	ggaggtgcag	gctgcagtgc	ccggcctgcc	aggccacgtc	aagtgtggca	2460
gtccaggtea	gctccagggc	cgagcatct	ttgcgcagga	tctgcgctc	tgctggatg	2520
aggccctctc	ctgggactgt	tttggcctct	cgctgctgac	cgtggccctg	ggcctggccg	2580

tgcccatgct gcaccacctc tgtggctggg acctctggta ctgcttccac ctgtgcctgg 2640  
 cctggctgcc ccggcggggg cgccggcggg gcgcggatgc cctgccctac gatgcctttg 2700  
 tggctcttga caaggcacag agcgcggtgg ccgactgggt gtacaacgag ctgcgggtac 2760  
 ggctagagga gcgccgtgga cgccgagcgc tccgcctgtg cctggaggaa cgtgactggc 2820  
 taccgggtaa aacgctcttt gagaacctgt gggcctcagt ttacagcagc cgcaagatgc 2880  
 tgtttgtgct ggccacaca gacaggggtca gcggcctctt gcgcgccagc tttctgctgg 2940  
 ccagcagcgc cctgctggag gaccgcaagg acgttgtggg gctggtgatc ctgcgccccg 3000  
 acgcccaccg ctcccgtat gtgcggctgc gccagcgcct ctgccgccag agcgtcctcc 3060  
 tctggcccca ccagcccagt ggccagcgca gcttctgggc ccagctgggc acggccctga 3120  
 ccagggacaa ccagcacttc tataaccaga acttctgccg gggcccccacg acggcagagt 3180  
 gaccgcccag caccocaagc ctctacacc ttgcctgtct gcctgggatg ccggg 3235

<210> 28

<211> 2460

<212> DNA

<213> Felis catus

<400> 28

atggggccct gccatgggc cctgcacccc ctgtctctcc tggcgcaggc tgccgcgctg 60  
 gccgtggccc tggcccaggg caccctgcct gcctttctgc cctgtgagct ccagcgccac 120  
 ggctggtga attgcgactg gctgttcctc aagtcgctgc ccacttctc ggcggcagcg 180  
 cccgtggta acgtcaccag cctttccctg tactccaacc gcatccacca cctccacgac 240  
 tccgactttg tccacctgtc cagcctgcgg cgtctcaacc tcaaattggaa ctgccacccc 300  
 gccagcctca gcccacatgca cttcccctgt cacatgacca ttgagcccca caccttctctg 360  
 gccgtgcccc ccctggagga gctgaacctg agctacaaca gcatcacgac agtaccgccc 420  
 ctgcccagtt ccctcgtgtc cctgtccttg agcgtacca acatcctggg gctggaccct 480  
 gccaacctcg cagggtgca ctccctgcgc tttctgttcc tggatggcaa ctgtactac 540  
 aagaacccct gccgcaggc cctgcagggt gcccggggcg cctccttgg cctgggcaac 600  
 cttacgcacc tgtactcaa gtacaacaac ctactgcgg tgccccgcgg cctgcccccc 660  
 agcctggagt acctgctatt gtcctacaac cacatcatca ccctggcacc tgaggacctg 720  
 gccaacctga ccgccctgcg tgtgctcgat gtgggtggga actgccgtcg ctgtgaccac 780  
 gcccgcaacc cctgtatgga gtgcccacag ggcttccgc acctgcaccc tgacaccttc 840  
 agccacctga accacctga aggcctggtg ttgaaggaca gctctctcta caacctgaac 900

```

cccagatggg tccatgccct gggcaacctc atgggtgctgg acctgagtga gaacttccta 960
tatgactgca tcacaaaaac cacagccttc cagggcctgg cccagctgcg cagactcaac 1020
ttgtctttca attaccacaa gaaggtgtcc ttgtcccacc tgcattctggc gccctccttc 1080
gggagcctgc tctccctgca gcagctggac atgcatggca tcttcttccg ctgctcagc 1140
gagaccacgc tccggctgct ggtccacctg cccatgctcc agagtctgca cctgcagatg 1200
aacttcatca atcaggccca gctcagcatc ttcggggcct tccctggcct gcgatacgtg 1260
gacctgtcag acaaccgcat aagtggagcc atggagctgg cggctgccac gggggaggtg 1320
gatgggtggg agagagtccg gctgccatct ggggacctag ctctggggcc accgggcacc 1380
cctagctccg agggcttcat gccaggctgc aagacctca acttcacctt ggacctgtca 1440
cggaacaacc tagtgacaat ccagccagag atgtttgccc ggctctcgcg cctccagtgc 1500
ctgctcctga gccgcaacag catctcgagc gcagtcaacg gctcacaatt tatgccgctg 1560
accagcctgc aggtgctgga cctgtcccat aacaagctgg acctgtacca tgggcgctct 1620
ttcacggagc tgccgaggct ggaggccctg gacctcagct acaacagcca gcccttcagc 1680
atgcagggcg tgggtcacaa cctcagcttt gtggcacagc tgccggccct gcgctatctc 1740
agcctggcgc acaacgacat ccacagccgt gtgtcccagc agctctgcag cgcctcgctg 1800
cgggccttgg acttcagcgg caatgccttg agccggatgt gggccgaggg agacctgtat 1860
ctccacttct tccgaggcct gaggagcctg gtccggttgg atctgtcca gaatcgctg 1920
cataccctct tgccacgcac cctggacaac ctccccaaga gcctgcggct gctgcgtctc 1980
cgtgacaatt atctggcttt cttcaactgg agcagcctgg tcctcctccc caggctggaa 2040
gccctggacc tggcgggaaa ccagctgaag gccctgagca acggcagctt gcctaattgga 2100
accagctcc agaggctgga cctcagcagc aacagtatca gcttcgtggc ctccagcttt 2160
tttgctctgg ccaccaggct gcgagagctc aaacctcagt ccaacgcctt caagacggtg 2220
gagccctcct gggttcgggtc tctagcgggc accctgaaag tcctagatgt gactggcaac 2280
cccctgcact gcgcctgtgg ggcggccttc gtggacttct tgctggaggt gcaggtgca 2340
gtgcccggcc tgccaggcca cgtcaagtgt ggcagtccag gtcagctcca gggccgcagc 2400
atctttgcgc aggatctgcg cctctgcctg gatgaggccc tctcctggga ctgttttggc 2460

```

```

<210> 29
<211> 1032
<212> PRT
<213> Mus musculus

```

&lt;400&gt; 29

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn  
 50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met  
 100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
 130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu

225		230		235		240
Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg						
	245			250		255
Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser						
	260		265			270
Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly						
	275		280			285
Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe						
	290		295		300	
Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu						
305		310		315		320
Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu						
	325			330		335
Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala						
	340		345			350
Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu						
	355		360			365
Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu						
	370		375			380
Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met						
385		390		395		400
Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala						
	405			410		415
Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr						
	420		425			430
Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu						
	435		440			445
Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser						
	450		455			460

Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu  
 465 470 475 480

Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
 485 490 495

Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala  
 500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp  
 515 520 525

Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu  
 530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
 545 550 555 560

Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser  
 565 570 575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val  
 580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly  
 595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe  
 610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn  
 625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu  
 645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr  
 660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn  
 675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
 690 695 700



Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala  
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn  
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn  
740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly  
755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly  
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg  
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser  
805 810 815

Trp Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val  
820 825 830

Val Pro Ile Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe  
835 840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser  
850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu  
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp  
900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr  
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser  
930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Phe Trp Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln  
 995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu  
 1025 1030

<210> 30  
 <211> 821  
 <212> PRT  
 <213> Mus musculus

<400> 30

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn  
 50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met  
 100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
 130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser  
 260 265 270

Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe  
 290 295 300

Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu  
 325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala

340	345	350
Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu		
355	360	365
Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu		
370	375	380
Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met		
385	390	400
Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala		
405	410	415
Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr		
420	425	430
Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu		
435	440	445
Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser		
450	455	460
Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu		
465	470	475
Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu		
485	490	495
Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala		
500	505	510
Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp		
515	520	525
Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu		
530	535	540
Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe		
545	550	555
Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser		
565	570	575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val  
580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly  
595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe  
610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn  
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu  
645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr  
660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn  
675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala  
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn  
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn  
740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly  
755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly  
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg  
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser  
805 810 815

Trp Asp Cys Phe Gly  
820

<210> 31

<211> 3200

<212> DNA

<213> Mus musculus

<400> 31

```

tgtcagaggg agcctcgggg gaatcctcca tctcccaaca tggttctccg tcgaaggact      60
ctgcaccctt tgtccctcct ggtacaggct gcagtgtctg ctgagactct ggccctgggt      120
accctgcctg ccttctctacc ctgtgagctg aagcctcatg gcctgggtgga ctgcaattgg      180
ctgttctctga agtctgtacc ccgtttctct gcggcagcat cctgtctcaa catcaccctgc      240
ctctccttga tctccaaccg tatccaccac ctgcacaact ccgacttctg ccacctgtcc      300
aacctgcggc agctgaacct caagtgggaa tgtccacca ctggccttag cccctgcac      360
ttctcttgcc acatgaccat tgagcccaga accttctctg ctatgcgtac actggaggag      420
ctgaacctga gctataatgg tatcaccact gtgccccgac tgcccagctc cctgggtgaat      480
ctgagcctga gccacaccaa catcctgggt ctagatgcta acagcctcgc cggcctatac      540
agcctgcgcg ttctcttcat ggacgggaa tgctactaca agaaccctg cacaggagcg      600
gtgaagggtga cccagggcg cctcctgggc ctgagcaatc tcaccatct gtctctgaag      660
tataacaacc tcacaaaggt gcccgcgcaa ctgcccccca gcctggagta cctcctgggtg      720
tcctataacc tcattgtcaa gctggggcct gaagacctgg ccaatctgac ctcccttcga      780
gtacttgatg tgggtgggaa ttgccgtcgc tgcgaccatg cccccaatcc ctgtatagaa      840
tgtggccaaa agtccctcca cctgcacct gagaccttcc atcacctgag ccatctggaa      900
ggcctgggtg tgaaggacag ctctctccat aactgaact cttcctgggt ccaaggctctg      960
gtcaacctct cggtgtctga cctaagcgag aactttctct atgaaagcat caaccacacc     1020
aatgcctttc agaacctaac ccgcctgcgc aagctcaacc tgtccttcaa ttaccgcaag     1080
aaggatcct ttgccgcct ccacctggca agttccttca agaacctggg gtcactgcag     1140
gagctgaaca tgaacggcat cttcttccgc tcgctcaaca agtacacgct cagatggctg     1200
gccgatctgc ccaaactcca cactctgcat cttcaaatga acttcatcaa ccaggcacag     1260
ctcagcatct ttggtacctt ccgagccctt cgctttgtgg acttgtcaga caatcgcatc     1320
agtgggcctt caacgctgtc agaagccacc cctgaagagg cagatgatgc agagcaggag     1380
gagctgttgt ctgcgatcc tcaccagct ccactgagca cccctgcttc taagaacttc     1440

```

atggacaggt gtaagaactt caagttcacc atggacctgt ctcggaacaa cctggtgact	1500
atcaagccag agatgtttgt caatctctca cgctccagt gtcttagcct gagccacaac	1560
tccattgcac aggctgtcaa tggctctcag ttctgcccgc tgactaatct gcaggtgctg	1620
gacctgtccc ataacaaact ggacttgtac cactggaaat cgttcagtga gctaccacag	1680
ttgcaggccc tggacctgag ctacaacagc cagcccttta gcatgaaggg tataggccac	1740
aatttcagtt ttgtggcca tctgtccatg ctacacagcc ttagcctggc acacaatgac	1800
attcataccc gtgtgtcctc acatctcaac agcaactcag tgaggtttct tgacttcagc	1860
ggcaacggta tgggccgcat gtgggatgag gggggccttt atctccattt cttccaaggc	1920
ctgagtggcc tgctgaagct ggacctgtct caaaataacc tgcatacct cggccccag	1980
aaccttgaca acctcccaa gagcctgaag ctgctgagcc tccgagacaa ctacctatct	2040
ttctttaact ggaccagtct gtccttctcg cccaacctgg aagtctaga cctggcaggc	2100
aaccagctaa aggccctgac caatggcacc ctgcctaata gcacctcct ccagaaactg	2160
gatgtcagca gcaacagtat cgtctctgtg gtcccagcct tcttcgctct ggcggtcgag	2220
ctgaaagagg tcaacctcag ccacaacatt ctcaagacgg tggatcgctc ctggtttggg	2280
cccattgtga tgaacctgac agttctagac gtgagaagca acctctgca ctgtgcctgt	2340
ggggcagcct tcgtagactt actgttggag gtgcagacca aggtgcctgg cctggctaata	2400
ggtgtgaagt gtggcagccc cggccagctg cagggccgta gcatcttcgc acaggacctg	2460
cggctgtgcc tggatgaggt cctctcttgg gactgctttg gcctttcact cttggtgtg	2520
gccgtgggca tgggtgtgcc tatactgcac catctctgcg gctgggacgt ctggtactgt	2580
tttcatctgt gcctggcatg gctacctttg ctggcccgca gccgacgcag cggccaagct	2640
ctcccctatg atgccttcgt ggtgttcgat aaggcacaga gcgcagttgc ggactgggtg	2700
tataacgagc tgcgggtgcg gctggaggag cggcgcggtc gccgagccct acgcttgtgt	2760
ctggaggacc gagattggct gcctggccag acgctcttcg agaacctctg ggcttccatc	2820
tatgggagcc gcaagactct atttgtgctg gccacacgg accgcgtcag tggcctcctg	2880
cgcaccagct tcctgctggc tcagcagcgc ctgttggaa accgcaagga cgtggtggtg	2940
ttggtgatcc tgcgtccgga tgcccaccgc tcccgtatg tgcgactgcg ccagcgtctc	3000
tgccgccaga gtgtgctctt ctggccccag cagcccaacg ggcagggggg cttctgggcc	3060
cagctgagta cagccctgac tagggacaac cgccacttct ataaccagaa cttctgcgg	3120
ggacctacag cagaatagct cagagcaaca gctggaaaca gctgcactct catgcctggt	3180
tcccagagtg ctctgcctgc	3200

<210> 32  
 <211> 2463  
 <212> DNA  
 <213> Mus musculus

<400> 32  
 atggttctcc gtcgaaggac tctgcacccc ttgtccctcc tggtagaggc tgcagtgtcg 60  
 gctgagactc tggccctggg taccctgcct gccttcctac cctgtgagct gaagcctcat 120  
 ggcctggtgg actgcaattg gctgttcctg aagtctgtac cccgtttctc tgcggcagca 180  
 tctgctcca acatcacccg cctctccttg atctccaacc gtatccacca cctgcacaac 240  
 tccgacttcg tccacctgtc caacctgcgg cagctgaacc tcaagtggaa ctgtccaccc 300  
 actggcctta gcccctgca cttctcttgc cacatgacca ttgagcccag aaccttctcg 360  
 gctatgcgta cactggagga gctgaacctg agctataatg gtatcaccac tgtgccccga 420  
 ctgcccagct ccctggtgaa tctgagcctg agccacacca acatcctggt tctagatgct 480  
 aacagcctcg ccggcctata cagcctgcgc gttctcttca tggacgggaa ctgctactac 540  
 aagaaccctc gcacaggagc ggtgaagggtg accccaggcg ccctcctggg cctgagcaat 600  
 ctcacccatc tgtctctgaa gtataacaac ctcacaaagg tgccccgcca actgcccccc 660  
 agcctggagt acctcctggt gtcctataac ctcatgttca agctggggcc tgaagacctg 720  
 gccaatctga cctcccttcg agtacttgat gtgggtggga attgccgtcg ctgcgaccat 780  
 gcccccaatc cctgtataga atgtggccaa aagtccctcc acctgcaccc tgagaccttc 840  
 catcacctga gccatctgga aggccctggtg ctgaaggaca gctctctcca tacactgaac 900  
 tcttcttggt tccaaggtct ggtcaacctc tcggtgctgg acctaaagca gaactttctc 960  
 tatgaaagca tcaaccacac caatgccttt cagaacctaa cccgcctgcg caagctcaac 1020  
 ctgtccttca attaccgcaa gaaggatatc tttgcccgcc tccacctggc aagttccttc 1080  
 aagaacctgg tgtcactgca ggagctgaac atgaacggca tcttcttccg ctgctcaac 1140  
 aagtacacgc tcagatggct ggccgatctg cccaaactcc acactctgca tcttcaaagt 1200  
 aacttcacat accaggcaca gctcagcatc tttggtagct tccgagccct tcgctttgtg 1260  
 gacttgtcag acaatcgcat cagtgggcct tcaacgctgt cagaagccac ccctgaagag 1320  
 gcagatgatg cagagcagga ggagctggtg tctgcggatc ctcacccagc tccactgagc 1380  
 acccctgctt ctaagaactt catggacagg tgtaagaact tcaagttcac catggacctg 1440  
 tctcggaaca acctggtgac tatcaagcca gagatgtttg tcaatctctc acgcctccag 1500  
 tgtcttagcc tgagccacaa ctccattgca caggctgtca atggctctca gttcctgccc 1560



ctgactaatc tgcaggtgct ggacctgtcc cataacaaac tggacttgta ccactggaaa 1620  
 tcgttcagtg agctaccaca gttgcaggcc ctggacctga gctacaacag ccagcccttt 1680  
 agcatgaagg gtataggcca caatttcagt tttgtggccc atctgtccat gctacacagc 1740  
 cttagcctgg cacacaatga cattcatacc cgtgtgtcct cacatctcaa cagcaactca 1800  
 gtgaggtttc ttgacttcag cggcaacggc atgggcccga tgtgggatga ggggggcctt 1860  
 tatctccatt tcttccaagg cctgagtggc ctgctgaagc tggacctgtc tcaaaaataac 1920  
 ctgcatatcc tccggcccca gaaccttgac aacctcccca agagcctgaa gctgctgagc 1980  
 ctccgagaca actacctatc tttctttaac tggaccagtc tgtccttcct gcccaacctg 2040  
 gaagtcctag acctggcagg caaccagcta aaggccctga ccaatggcac cctgcctaata 2100  
 ggcacctctc tccagaaact ggatgtcagc agcaacagta tcgtctctgt ggtcccagcc 2160  
 ttcttcgctc tggcggtcga gctgaaagag gtcaacctca gccacaacat tctcaagacg 2220  
 gtggatcgct cctggtttgg gccatttgat atgaacctga cagttctaga cgtgagaagc 2280  
 aacctctctg actgtgcctg tggggcagcc ttcgtagact tactgttgga ggtgcagacc 2340  
 aaggtgcctg gcctggctaa tgggtgtgaag tgtggcagcc ccggccagct gcagggccgt 2400  
 agcatcttcg cacaggacct gcggctgtgc ctggatgagg tcctctcttg ggactgcttt 2460  
 ggc 2463

<210> 33  
 <211> 1032  
 <212> PRT  
 <213> Homo sapiens

<400> 33

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp  
                                     85                                    90                                    95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met  
                                     100                                    105                                    110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
                                     115                                    120                                    125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser  
                                     130                                    135                                    140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser  
                                     145                                    150                                    155                                    160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly  
                                     165                                    170                                    175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro  
                                     180                                    185                                    190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
                                     195                                    200                                    205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr  
                                     210                                    215                                    220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu  
                                     225                                    230                                    235                                    240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
                                     245                                    250                                    255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe  
                                     260                                    265                                    270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
                                     275                                    280                                    285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe  
                                     290                                    295                                    300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu

305                      310                      315                      320  
 Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu  
                                  325                                   330                                   335  
 Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala  
                                  340                                   345                                   350  
 His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu  
                                  355                                   360                                   365  
 Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu  
                                  370                                   375                                   380  
 Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met  
                                  385                                   390                                   395                                   400  
 Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly  
                                  405                                   410                                   415  
 Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu  
                                  420                                   425                                   430  
 Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu  
                                  435                                   440                                   445  
 Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu  
                                  450                                   455                                   460  
 Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser  
                                  465                                   470                                   475                                   480  
 Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser  
                                  485                                   490                                   495  
 His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val  
                                  500                                   505                                   510  
 Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu  
                                  515                                   520                                   525  
 Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu  
                                  530                                   535                                   540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly  
545 550 555 560

Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr  
565 570 575

Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser  
580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
595 600 605

Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe  
610 615 620

Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu  
625 630 635 640

His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln  
645 650 655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser  
660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg  
675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg  
690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe  
705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu  
740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu  
770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser  
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp  
805 810 815

Asp Cys Phe Ala Leu Ser Leu Leu Ala Val Ala Leu Gly Leu Gly Val  
820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His  
835 840 845

Leu Cys Leu Ala Trp Leu Pro Trp Arg Gly Arg Gln Ser Gly Arg Asp  
850 855 860

Glu Asp Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Thr Gln  
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Gly Gln Leu Glu  
885 890 895

Glu Cys Arg Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp  
900 905 910

Trp Leu Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr  
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser  
930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Gly Arg  
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln  
995 1000 1005

Leu Gly Met Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg  
1010 1015 1020

Asn Phe Cys Gln Gly Pro Thr Ala Glu  
1025 1030

<210> 34  
<211> 820  
<212> PRT  
<213> Homo sapiens

<400> 34

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn  
50 55 60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp  
65 70 75 80

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met  
100 105 110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
115 120 125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser  
130 135 140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser  
145 150 155 160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly  
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro  
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe  
 260 265 270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe  
 290 295 300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu  
 325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala  
 340 345 350

His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu  
 370 375 380

Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu

420	425	430
Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu		
435	440	445
Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu		
450	455	460
Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser		
465	470	475
Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser		
485	490	495
His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val		
500	505	510
Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu		
515	520	525
Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu		
530	535	540
Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly		
545	550	555
Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr		
565	570	575
Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser		
580	585	590
Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn		
595	600	605
Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe		
610	615	620
Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu		
625	630	635
His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln		
645	650	655



Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser  
660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg  
675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg  
690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe  
705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu  
740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu  
770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser  
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp  
805 810 815

Asp Cys Phe Ala  
820

<210> 35  
<211> 3352  
<212> DNA  
<213> Homo sapiens

<400> 35  
aggctggtat aaaaatctta cttoctctat tctctgagcc gctgctgccc ctgtgggaag 60  
ggacctcgag tgtgaagcat ccttcctgt agctgctgtc cagtctgccc gccagaccct 120  
ctggagaagc ccttgccccc cagcatgggt ttctgccgca gcgccctgca cccgctgtct 180  
ctcctgggtgc aggccatcat gctggccatg accctggccc tgggtacctt gctgccttc 240  
ctaccctgtg agctccagcc ccacggcctg gtgaactgca actggctgtt cctgaagtct 300

gtgccccact tctccatggc agcaccocgt ggcaatgtca ccagcctttc cttgtcctcc 360  
 aaccgcatcc accacctcca tgattctgac tttgcccacc tgcccagcct gcggcatctc 420  
 aacctcaagt ggaactgccc gccggttggc ctcagcccca tgcacttccc ctgccacatg 480  
 accatcgagc ccagcacctt cttggctgtg cccaccctgg aagagctaaa cctgagctac 540  
 aacaacatca tgactgtgcc tgcgtgccc aaatccctca tatccctgtc cctcagccat 600  
 accaacatcc tgatgctaga ctctgccagc ctgcgggcc tgcatgccct gcgcttccta 660  
 ttcattggacg gcaactgtta ttacaagaac ccctgcaggc aggcactgga ggtggccccg 720  
 ggtgcccctc ttggcctggg caacctcacc cacctgtcac tcaagtacaa caacctcact 780  
 gtggtgcccc gcaacctgcc ttccagcctg gagtatctgc tgttgtccta caaccgcatc 840  
 gtcaaactgg cgctgagga cctggccaat ctgaccgccc tgcgtgtgct cgatgtgggc 900  
 ggaaattgcc gccgtgcga ccacgtccc aaccctgca tggagtggc tcgtcacttc 960  
 cccagctac atcccgatac cttcagccac ctgagccgtc ttgaaggcct ggtgttgaag 1020  
 gacagttctc tctcctggct gaatgccagt tggttccgtg ggctgggaaa cctccgagt 1080  
 ctggacctga gtgagaactt cctctacaaa tgcatacta aaaccaaggc cttccagggc 1140  
 ctaacacagc tgcgcaagct taacctgtcc ttcaattacc aaaagagggt gtcctttgcc 1200  
 cacctgtctc tggccccttc cttcgggagc ctggtcgccc tgaaggagct ggacatgcac 1260  
 ggcatcttct tccgctcact cgatgagacc acgctccggc cactggcccc cctgcccattg 1320  
 ctccagactc tgcgtctgca gatgaacttc atcaaccagg cccagctcgg catcttcagg 1380  
 gccttccctg gcctgcgcta cgtggacctg tcggacaacc gcatcagcgg agcttcggag 1440  
 ctgacagcca ccatggggga ggcagatgga ggggagaagg tctggctgca gcctggggac 1500  
 cttgtccggg cccagtgga cactcccagc tctgaagact tcaggcccaa ctgcagcacc 1560  
 ctcaacttca ccttgatct gtcacggaac aacctggta cctgcagcc ggagatgttt 1620  
 gccagctct cgacactgca gtgcctgcgc ctgagccaca actgcatctc gcaggcagtc 1680  
 aatggctccc agttcctgcc gctgaccggt ctgcaggtgc tagacctgtc ccgcaataag 1740  
 ctggacctct accacgagca ctcatcagc gagctaccgc gactggaggc cctggacctc 1800  
 agctacaaca gccagccctt tggcatgcag ggcgtgggcc acaacttcag cttcgtggct 1860  
 cacctgcgca ccctgcgcca cctcagcctg gccacaaca acatccacag ccaagtgtcc 1920  
 cagcagctct gcagtacgtc gctgcgggcc ctggacttca gcggcaatgc actgggccat 1980  
 atgtgggccc agggagacct ctatctgcac ttcttccaag gcctgagcgg tttgatctgg 2040

ctggacttgt cccagaaccg cctgcacacc ctccctgccc aaaccctgcg caacctcccc 2100  
 aagagcctac aggtgctgcg tctccgtgac aattacctgg ccttctttaa gtggtggagc 2160  
 ctccacttcc tgcccaaact ggaagtcctc gacctggcag gaaaccggct gaaggccctg 2220  
 accaatggca gcctgcctgc tggcaccggg ctccggaggc tggatgtcag ctgcaacagc 2280  
 atcagcttcg tggcccccg cttcttttcc aaggccaagg agctgcgaga gctcaacctt 2340  
 agcgccaacg ccctcaagac agtggaccac tcttggtttg ggccctggc gagtgccctg 2400  
 caaatactag atgtaagcgc caaccctctg cactgcgcct gtggggcggc ctttatggac 2460  
 ttcctgctgg aggtgcaggc tgccgtgccc ggtctgcca gccgggtgaa gtgtggcagt 2520  
 ccgggccagc tccagggcct cagcatcttt gcacaggacc tgcgcctctg cctggatgag 2580  
 gccctctcct gggactgttt cgccctctcg ctgctggctg tggctctggg cctgggtgtg 2640  
 cccatgctgc atcacctctg tggctgggac ctctggtact gcttccacct gtgcctggcc 2700  
 tggcttccct ggcgggggcg gcaaagtggg cgagatgagg atgcctgcc ctacgatgcc 2760  
 ttcgtggtct tcgacaaaac gcagagcgca gtggcagact ggggtgtacaa cgagcttcgg 2820  
 gggcagctgg aggagtgcg tgggcgctgg gcaactccgc tgtgcctgga ggaacgcgac 2880  
 tggctgcctg gcaaaaccct ctttgagaac ctgtgggcct cggctctatgg cagccgcaag 2940  
 acgctgtttg tgctggccca cacggaccgg gtcagtggc tcttgcgcg cagcttccctg 3000  
 ctggcccagc agcgccctgct ggaggaccgc aaggacgtcg tgggtgctgg gatcctgagc 3060  
 cctgacggcc gccgctcccc ctacgtgcgg ctgcgccagc gcctctgcc ccagagtgtc 3120  
 ctctctggc cccaccagcc cagtggtcag cgcagcttct gggcccagct gggcatggcc 3180  
 ctgaccaggg acaaccacca cttctataac cggaacttct gccagggacc cacggccgaa 3240  
 tagccgtgag ccggaatcct gcaagggtgc acctccacac tcacctcacc tctgcctgcc 3300  
 tggcttgacc ctccctgct cgctccctc accccacacc tgacacagag ca 3352

<210> 36  
 <211> 2460  
 <212> DNA  
 <213> Homo sapiens

<400> 36  
 atgggtttct gccgcagcgc cctgcacccg ctgtctctcc tgggtgcaggc catcatgctg 60  
 gccatgacct tggccctggg taccttgcc gccttcctac cctgtgagct ccagccccac 120  
 ggcttggtga actgcaactg gctgttctcg aagtctgtgc ccacttctc catggcagca 180  
 cccgtggca atgtcaccag ctttccctg tctccaacc gcatccacca cctccatgat 240

tctgactttg cccacctgcc cagcctgcgg catctcaacc tcaagtggaa ctgcccgcg	300
gttggcctca gcccacatgca cttccccctgc cacatgacca tcgagcccag caccttcttg	360
gctgtgccc aacctggaaga gctaaacctg agctacaaca acatcatgac tgtgcctgcg	420
ctgccccaaat ccctcatatc cctgtccctc agccatacca acatcctgat gctagactct	480
gccagcctcg ccggcctgca tgcctgcgc ttcctattca tggacggcaa ctgttattac	540
aagaacccct gcaggcaggc actggagggtg gcccgggtg ccctccttg cctgggcaac	600
ctcaccaccc tgtcactcaa gtacaacaac ctactgttg tgcgccgcaa cctgccttcc	660
agcctggagt atctgctgtt gtccataaac cgcctgtca aactggcgcc tgaggacctg	720
gccaatctga ccgccctgcg tgtgctcgat gtgggcggaa attgccgcg ctgcgaccac	780
gtcccaacc cctgcatgga gtgcctcgt cacttcccc agctacatcc cgataccttc	840
agccacctga gccgtcttga aggcctggtg ttgaaggaca gttctctctc ctggctgaat	900
gccagttggt tccgtgggt gggaaacctc cgagtgttg acctgagtga gaacttctc	960
tacaaatgca tactaaaaac caaggccttc cagggcctaa cacagctgcg caagcttaac	1020
ctgtccttca attacaaaaa gaggggtgtcc tttgccacc tgtctctggc cccttcttc	1080
gggagcctgg tcgccctgaa ggagctggac atgcacggca tcttcttcg ctactcgat	1140
gagaccacgc tccggccact ggccgcctg cccatgtcc agactctgcg tctgcagatg	1200
aacttcatca accaggccca gctcggcatc ttcaggcct tccctggcct gcgctacgtg	1260
gacctgtcgg acaaccgcat cagcggagt tcggagctga cagccaccat gggggaggca	1320
gatggagggg agaaggctctg gctgcagcct ggggacctt ctccggcccc agtggacact	1380
cccagctctg aagacttcag gcccaactgc agcaccctca acttcacctt ggatctgtca	1440
cggaacaacc tggtgaccgt gcagccggag atgtttgcc agctctcgca cctgcagtgc	1500
ctgcgcctga gccacaactg catctcgag gcagtcaatg gctcccagtt cctgccgctg	1560
accggtctgc aggtgctaga cctgtccgc aataagctgg acctctacca cgagcactca	1620
ttcacggagc taccgcgact ggaggccctg gacctcagct acaacagcca gccctttggc	1680
atgcagggcg tgggccacaa cttcagcttc gtggctcacc tgcgaccct gcgccacctc	1740
agcctggccc acaacaacat ccacagccaa gtgtcccagc agctctgcag tacgtcgctg	1800
cgggccctgg acttcagcgg caatgcactg ggccatatgt gggccgagg agacctctat	1860
ctgcacttct tccaaggcct gagcggtttg atctggctgg acttgtccca gaaccgcctg	1920
cacaccttcc tgcccaaac cctgcgcaac ctcccaaga gcctacaggt gctgcgtctc	1980
cgtgacaatt acctggcctt ctttaagtgg tggagcctcc acttctgcc caaactggaa	2040

gtcctcgacc tggcaggaaa cgggctgaag gccctgacca atggcagcct gcctgctggc 2100  
 acccggtccc ggaggctgga tgcagctgc aacagcatca gcttcgtggc ccccggttc 2160  
 ttttccaagg ccaaggagct gcgagagctc aaccttagcg ccaacgccct caagacagtg 2220  
 gaccactcct ggtttgggcc cctggcgagt gccctgcaaa tactagatgt aagcgccaac 2280  
 cctctgcact ggcctgtgg ggcgccctt atggacttcc tgctggaggt gcaggctgcc 2340  
 gtgcccggtc tgcccagccg ggtgaagtgt ggcagtccg gccagctcca gggcctcagc 2400  
 atctttgcac aggacctgcg cctctgcctg gatgaggccc tctcctggga ctgtttcgcc 2460

<210> 37

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 37

accttgctg ccttctacc ctgtga

26

<210> 38

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 38

gtccgtgtgg gccagcaca a

21

<210> 39

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 39

tccatgacgt ttttgatgtt

20

<210> 40

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 40  
tccataacgt ttttgatggt 20

<210> 41  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 41  
tccatcacgt ttttgatggt 20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 42  
tccattacgt ttttgatggt 20

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 43  
tccatggcgt ttttgatggt 20

<210> 44  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 44  
tccatgccgt ttttgatggt 20

<210> 45  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 45

tccatgctcg ttttgatggt

20

<210> 46

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 46

tccatgatgt ttttgatggt

20

<210> 47

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 47

tccatgaagt ttttgatggt

20

<210> 48

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 48

tccatgaggt ttttgatggt

20

<210> 49

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 49

tccatgacat ttttgatggt

20

<210> 50

<211> 20

<212> DNA

<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 50  
tccatgacct ttttgatggt 20

<210> 51  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 51  
tccatgactt ttttgatggt 20

<210> 52  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 52  
tccatgacgc ttttgatggt 20

<210> 53  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 53  
tccatgacga ttttgatggt 20

<210> 54  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 54  
tccatgacgg ttttgatggt 20

<210> 55  
<211> 20  
<212> DNA  
<213> Artificial sequence



<220>  
<223> Synthetic oligonucleotide

<400> 55  
tccatgacgt ctttgatggt 20

<210> 56  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 56  
tccatgacgt atttgatggt 20

<210> 57  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 57  
tccatgacgt gtttgatggt 20

<210> 58  
<211> 24  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 58  
tcgctgctttt gtcgcttttgt cggt 24

<210> 59  
<211> 24  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 59  
tgctgctttt gtgcttttgt gctt 24

<210> 60  
<211> 20  
<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 60

tccatgacgt tcctgatgct

20

<210> 61

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 61

tccatgagct tcctgatgct

20

<210> 62

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> Consensus oligopeptide

<220>

<221> MISC\_FEATURE

<222> (4)..(5)

<223> Any amino acid

<220>

<221> MISC\_FEATURE

<222> (7)..(12)

<223> Any amino acid

<220>

<221> MISC\_FEATURE

<222> (14)..(15)

<223> Any amino acid

<400> 62

Gly Asn Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys  
1 5 10 15

<210> 63

<211> 16

<212> PRT

<213> Homo sapiens

<400> 63

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys  
 1 5 10 15

<210> 64  
 <211> 16  
 <212> PRT  
 <213> Mus musculus

<400> 64

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Ile Cys  
 1 5 10 15

<210> 65  
 <211> 31  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <223> Consensus oligopeptide

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 65

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Asp Xaa Tyr Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Ser Xaa Xaa Xaa Xaa Xaa Xaa Tyr  
 20 25 30

<210> 66  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 66

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Tyr  
 20 25 30

<210> 67  
 <211> 31  
 <212> PRT  
 <213> Mus musculus

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 67

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Gln Leu Xaa Xaa Xaa Xaa Xaa Xaa Tyr  
 20 25 30

<210> 68  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<400> 68

Gln Val Leu Asp Leu Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His  
 1 5 10 15

Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr  
 20 25 30

<210> 69  
 <211> 31  
 <212> PRT  
 <213> Mus musculus

<400> 69

Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys

1

5

10

15

Ser Phe Ser Glu Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr  
20 25 30

&lt;210&gt; 70

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide

&lt;400&gt; 70

tccaggactt ctctcaggtt

20